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OM protein - protein search, using sw model

Run on: July 3, 2004, 05:12:17 ; Search time 34.8113 Seconds
(without alignments)

Title: US-10-088-092A-30_COPY_20_142

Perfect score: 722

Sequence: 1 NLVQFGTMIEKNTGKSALQY.....YNRKYAHYPNKLCTGPTPPC 123

Scoring table: BL05M62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04;*

- 1: GeneseqP1980s;*
- 2: GeneseqP1980s;*
- 3: GeneseqP2000s;*
- 4: GeneseqP2001s;*
- 5: GeneseqP2002s;*
- 6: GeneseqP2003as;*
- 7: GeneseqP2003bs;*
- 8: GeneseqP2004s;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	722	100.0	142	4	AAB81022	Aab81022 Human pho
2	722	100.0	154	6	ABR44235	Abr44235 Human sec
3	722	100.0	154	6	ABU63125	Abu63125 Human gro
4	662	91.7	142	3	AAB12810	Aab12810 Mouse sec
5	662	91.7	142	4	AAB81021	Aab81021 Murine ph
6	363.5	50.3	124	5	ADA61984	Ad61984 Human t8m
7	360.5	49.9	124	5	AAR10126	Aar10126 Membrane-
8	360.5	49.9	124	5	AAW73562	Aaw73562 Human gro
9	360.5	49.9	124	6	ADA61982	Ad61982 Human G72
10	360.5	49.9	124	6	ADA61978	Ad61978 Human G72
11	360.5	49.9	124	6	ABR83569	Ab83569 Human PLA
12	360.5	49.9	144	6	AAP93112	Aap93112 Human inf
13	360.5	49.9	144	1	AAP93163	Aap93163 Human syn
14	360.5	49.9	144	2	AAR25416	Aar25416 PLA.
15	360.5	49.9	144	2	AAR61055	Aar61055 Human PLA
16	360.5	49.9	144	6	ABR44233	Abr44233 Human sec
17	360.5	49.9	144	6	ABP98607	Abp98607 Human pho
18	360.5	49.9	144	6	ABU63123	Abu63123 Human gro
19	360.5	49.9	144	7	ADB75501	Adb75501 Prostate
20	360.5	49.9	144	7	ADE63560	Ade63560 Human pro
21	360.5	49.9	164	3	AAB56432	Ada56432 Human pro
22	357.5	49.5	124	6	ADA61983	Ad61983 Human T10
23	348	48.2	125	2	AAR61060	Aar61060 Rat PLA
24	347	48.1	146	2	ADE33558	Ade33558 Rat Prote
25	341	47.2	146	2	Aaw08368	Aaw08368 Mouse PLA

ALIGNMENTS

RESULT 1	
ID	AAB81022
XX	XX
AC	AC
DT	12-JUN-2001 (first entry)
XX	XX
DE	Human phospholipase A2 (PLA2) amino acid sequence.
XX	Phospholipase A2; PLA2; antibacterial; immunosuppressive; vulnerability; antiinflammatory; antiarthritic; septic shock; pancreatic; human; adult respiratory distress syndrome; ARDS; bronchial asthma; allergic rhinitis; rheumatoid arthritis.
XX	KW
OS	Homo sapiens.
XX	Location/Qualifiers
PH	1: 1.19
FT	/label= Signal_peptide
FT	20: 1.142
FT	/label= Mature_PLA2
FT	/note= "Mature phospholipase A2"
XX	WO200121775-A1.
XX	WO200121775-A1.
XX	PD 29-MAR-2001.
XX	XX
PF	18-SEP-2000; 2000WO-JP006344.
XX	XX
PF	21-SEP-1999; 99JP-00266616.
XX	XX
PA	(SHIO) SHIONOGI & CO LTD.
XX	XX
PI	Ishizaki J, Suzuki N, Hanasaki K;
XX	XX
DR	WPI; 2001-290422/30.
DR	N-PSDB; AAF77401.
XX	XX
PT	Human secretory phospholipase A2 and encoded gene, useful in diagnosis of
PT	and screening drug candidates for treating associated diseases e.g.
PT	septic shock, adult respiratory distress syndrome and rheumatoid
PT	arthritis.
PS	Claim 1; Page 46-47; 50PP; Japanese.
XX	This invention relates to human secretory phospholipase A2 (PLA2) protein
CC	

CC and the gene encoding it. Inhibitors of phospholipase A2 have
 CC antibacterial; immunosuppressive; antinflammatory; tranquiliser;
 CC antiasthmatic; analgesic; antiarthritic;
 CC vulnerability. The PLA2 protein, gene and anti-PLA2 antibody are useful in
 CC the diagnosis of PLA2 associated diseases e.g. septic shock, adult
 CC respiratory distress syndrome, pancreatitis, trauma, bronchial asthma,
 CC allergic rhinitis and rheumatoid arthritis. The present sequence
 CC represents human PLA2
 XX Sequence 142 AA;

Query Match	100.0%	Score 722;	DB 4;	Length 142;
Best Local Similarity	100.0%	Pkd. No. 8	5e-59;	
Matches 123;	Conservative 0;	Indels 0;	Gaps 0;	
Qy	1 NLVQGVMIEKMTGKSALQNDYGGCGIGGSHMPVDQTDWCCCHAHDCCYGRLEKLGCEP	60		
Db	20 NLVQGVMIEKMTGKSALQNDYGGCGIGGSHMPVDQTDWCCCHAHDCCYGRLEKLGCEP	79		
Qy	61 KLEYKLFPSVBERGFCAAGTTTCQRLTCECDKRAALCFRNLGLTYNRKYAHYPNKLCTGPT	120		
Db	80 KLEYKLFPSVBERGFCAAGTTTCQRLTCECDKRAALCFRNLGLTYNRKYAHYPNKLCTGPT	139		
Qy	121 PPC 123			
Db	140 PPC 142			

RESULT 2
 ABR44235 standard; protein; 154 AA.
 XX ABR44235;

XX DT 18-AUG-2003 (first entry)

DE Human secreted group IIF phospholipase A2 (sPLA2) enzyme.
 XX Group IIF secreted phospholipase A2; sPLA2; phosphatidylglycerol; human;

KW phosphatidylcholine; antibacterial; virucide; vasoconstrictive; vasoconstrictive;
 KW antiinflammatory; vasoconstrictive; cytosolic; vasoconstrictive;
 KW chromosome 1p35; transgenic; enzyme.

OS Homo sapiens.

XX WO2003033689-A1.
 XX PN 24-APR-2003.

XX PP 12-OCT-2001; 2001WO-1B002407.
 XX PR 12-OCT-2001; 2001WO-1B002407.

XX PA (CNRS) CNRS CENT NAT RECH SCI.

XX PI Lazdunski M, Lambeau G, Valentin E;
 XX DR; 2003-403216/38.

XX Novel mammalian secreted group IIF secreted phospholipase A2, useful for
 PT preventing and treating bacterial and viral infections, and cancers.
 XX Disclosure; Fig 1; 33pp; English.
 XX The invention relates to a mammalian secreted group IIF secreted
 CC phospholipase A2 (sPLA2) (I), where the enzyme is Ca²⁺ dependent,
 CC maximally active at pH 7-8 and hydrolyzes phosphatidylglycerol versus
 CC phosphatidylcholine with a 15-fold preference. A pharmaceutical composition
 CC comprising (I) is useful for treating or preventing viral and
 CC bacterial infections, and cancers. A pharmaceutical composition
 CC containing compounds capable of inhibiting catalytic activity of (I),
 CC biologically active compounds that bind sPLA₂ receptors, or a compound
 CC that modulates cell proliferation, cell migration, cell contraction or

CC apoptosis is useful for treating disease states or disorders involving
 CC group IIF sPLA2, such as inflammatory disease, cancers, cardiac and brain
 CC ischaemia, acute lung injury, acute respiratory distress syndrome or
 CC Crohn's disease. Specific antibodies are useful for searching new
 CC secreted mammalian group IIF sPLA2 or the homologues of the enzyme in
 CC other mammals. The encoding polynucleotides and vectors are useful for
 CC transforming animals and establishing a line of transgenic animals.
 CC Sequences ABR44232-239 represent various human secreted sPLA2 enzymes
 CC used in alignment studies with the GIIF sPLA2 enzyme
 XX SQ Sequence 154 AA;

Query Match	100.0%;	Score 722;	DB 6;	Length 154;
Best Local Similarity	100.0%;	Pred. No. 9.e-59;		
Matches 123;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1 NLVQGVMIEKMTGKSALQNDYGGCGIGGSHMPVDQTDWCCCHAHDCCYGRLEKLGCEP	60		
Db	32 NLVQGVMIEKMTGKSALQNDYGGCGIGGSHMPVDQTDWCCCHAHDCCYGRLEKLGCEP	91		
Qy	61 KLEYKLFPSVBERGFCAAGTTTCQRLTCECDKRAALCFRNLGLTYNRKYAHYPNKLCTGPT	120		
Db	92 KLEYKLFPSVBERGFCAAGTTTCQRLTCECDKRAALCFRNLGLTYNRKYAHYPNKLCTGPT	151		
Qy	121 PPC 123			
Db	152 PPC 154			

RESULT 3
 ABU63125
 ID ABU63125 standard; protein; 154 AA.
 XX AC ABU63125;
 XX DT 25-SEP-2003 (first entry)

DE Human group IIE secreted phospholipase A2.
 XX Human; group IIE secreted phospholipase A2; virucide; antibacterial;
 KW cytostatic; antiinflammatory; vasoconstrictive; sPLA2;
 KW phosphatidylglycerol hydrolysis; phosphatidylcholine hydrolysis;
 KW viral infection; bacterial infection; cancer; inflammatory disease;
 KW cardiac ischaemia; brain ischaemia; acute lung injury;
 KW acute respiratory distress syndrome; Crohn's disease; enzyme.
 XX OS Homo sapiens.

XX PN US2003073087-A1.
 XX PD 17-APR-2003.

XX PF 11-OCT-2001; 2001US-0097556.
 XX PR 11-OCT-2000; 2000US-0239491P.

XX PA (LAZDUNSKI M.
 XX PA (LAMB /) LAMBEAU G.
 XX PA (VALE /) VALENTIN E.

XX PI Lazdunski M, Lambeau G, Valentin E;

XX DR; 2003-567302/53.

XX New mammalian secreted group IIF phospholipase A2 or nucleic acid, useful
 PT for treating or preventing viral or bacterial infections, or cancers, or
 PT screening inhibitors of the enzyme for treating e.g. inflammatory
 PT diseases or ischaemia.
 XX Disclosure; Fig 1; 16pp; English.
 XX The invention describes a mammalian secreted group IIF phospholipase A2
 CC (sPLA2), which is Ca²⁺-dependent, maximally active at pH of about 7-8,
 CC that modulates cell proliferation, cell migration, cell contraction or

CC Group IIA PLA2 and an antibiotic; The methods of the invention are useful
 CC for killing Gram-positive bacteria, (especially *Staphylococcus aureus*)
 CC and for treating human patient suffering from an infection caused by Gram
 CC -positive bacteria. The bacteria are selected from Micrococcus,
 CC *Staphylococcus*, *Peptococcus*, *Lactobacillus*,
 CC *Enterococcus*, *Methanobacterium*, *Bacillus*, *Clostridium*, *Propionibacterium*,
 CC *Listeria*, *Erysipelothrix*, *Corynebacterium*, *Bifidobacterium*, *Bacterioides*,
 CC *Bacillus*, *Actinomyces*, *Archaea*, *Streptomyces* and *Micrococcaceae*. The
 CC *Rothia*, *Mycobacterium*, *Nocardioides*, *Streptomyces* and *Micrococcaceae*. The
 CC methods are useful for treating potentially life-threatening infection
 CC caused by multi-drug resistant Gram positive bacteria, for treating wound
 CC and bloodstream infection with methicillin-resistant *S. aureus* (MRSA) and
 CC nosocomial infections with vancomycin-resistant *Enterococcus faecium*. The
 CC present sequence represents the 18M/G2K/T103K mutant PLA2 of the
 CC invention. Note: The present sequence is not shown in the specification
 CC but was created by the indexer using the information in example 1 and the
 CC sequence appearing as ADA61978.
 XX Sequence 142 AA;
 SQ Sequence 124 AA;
 Query Match 91.7%; Score 662; DB 4; Length 142;
 Best Local Similarity 88.6%; Pred. No. 2 8e-53;
 Matches 109; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
 Qy 1 NLVQFGVMTEKMTGKSLQNDYCGCGIGSHWPVDOTDWCCCHAHDCCYGRLEKGCEP 60
 Db 20 NLVQFGWMTRMTGKPALQNDYCGCGIGSHWPVDOTDWCCCHAHDCCYGRLEKGCDP 79
 Qy 61 KLERXLFISVERGIFCAAGTTCQRLTCECDKRALCFFRNLYGTYRKAHYPNKLCTGPT 120
 Db 80 KLERXLFISVERGIFCAAGTTCQRLTCECDKRALCFFRNLYGTYRKAHYPNKLCTGPT 139
 Qy 121 PPC 123
 Db 140 PPC 142
 Query Match 50.3%; Score 363.5; DB 6; Length 124;
 Best Local Similarity 55.6%; Pred. No. 7.5e-26;
 Matches 69; Conservative 10; Mismatches 44; Indels 1; Gaps 1;
 Qy 1 NLVQFGVMIEKMTGKSLQNDYCGCYGIGSHWPVDOTDWCCCHAHDCCYGRLEKGCE 59
 Db 1 NLVNFRMIRMIKLTGREALSYGFVGCHCGVGRESPKDADTRCCVTHDCYRKLEKRCG 60
 Qy 60 PKELEYTLFSVERGIFCAAGTTCQRLTCECDKRALCFFRNLYGTYRKAHYPNKLCTGP 119
 Db 61 TKFLSYKPSNSKSRSITCAKQDSRSQCECDKAATCFARNKTYKQYYSNKHCRGS 120
 XX Synthesis:
 OS Synthetic.
 OS Homo sapiens.
 FH Location/Qualifiers
 FT Misc-difference 8 /note= "Wild-type Ile substituted by Met"
 FT Misc-difference 72 /note= "Wild-type Gly substituted by Lys"
 FT Misc-difference 103 /note= "Wild-type Thr substituted by Lys"
 XX PN US6475484-B1.
 XX PD 05-NOV-2002.
 XX PP 18-DEC-2000; 2000US-00740569.
 XX PR 17-DEC-1999; 99US-0172467P.
 XX PA (UNIV) UNIV NEW YORK STATE.
 XX PI Weiss J, Elsbach P, Liang N;
 XX DR WPI; 2003-219013/21.
 XX PT Treating a patient suffering from infection caused by gram-positive
 PT bacteria or killing gram-positive bacteria, comprises delivering mutant
 PT human Group IIA phospholipase A2.
 XX Example 1; Page: 22PP; English.
 XX CC The invention relates to killing gram-positive bacteria (I) in human
 CC patient, comprising contacting the bacteria with a bactericidal-effective
 CC amount of mutant human Group IIA phospholipase A2 (Group IIA PLA2)
 CC appearing as ADA61978, or treating a human patient suffering from
 CC infection caused by a bacteria comprising administering a mutant human
 XX

RESULT 6
 ADA61984 standard; protein; 124 AA.
 XX AC ADA61984;
 XX DT 20-NOV-2003 (first entry)
 XX DE Human 18M/G72K/T103K PLA2 mutant.
 XX KW -Antibacterial; gram-positive bacteria; human; group IIA phospholipase A2;
 KW group IIA PLA2; bacterial infection; *Staphylococcus aureus*;
 KW multi-drug resistance; wound; bloodstream infection;
 KW methicillin-resistant *S. aureus*; MRSA; nosocomial infection;
 KW vancomycin-resistant *Enterococcus faecium*; mutein; mutant.
 XX
 OS Synthetic.
 OS Homo sapiens.
 FH Location/Qualifiers
 FT Misc-difference 8 /note= "Wild-type Ile substituted by Met"
 FT Misc-difference 72 /note= "Wild-type Gly substituted by Lys"
 FT Misc-difference 103 /note= "Wild-type Thr substituted by Lys"
 XX PN US6475484-B1.
 XX PD 05-NOV-2002.
 XX PP 18-DEC-2000; 2000US-00740569.
 XX PR 17-DEC-1999; 99US-0172467P.
 XX PA (UNIV) UNIV NEW YORK STATE.
 XX PI Weiss J, Elsbach P, Liang N;
 XX DR WPI; 2003-219013/21.
 XX PT Treating a patient suffering from infection caused by gram-positive
 PT bacteria or killing gram-positive bacteria, comprises delivering mutant
 PT human Group IIA phospholipase A2.
 XX Example 1; Page: 22PP; English.
 XX CC The invention relates to killing gram-positive bacteria (I) in human
 CC patient, comprising contacting the bacteria with a bactericidal-effective
 CC amount of mutant human Group IIA phospholipase A2 (Group IIA PLA2)
 CC appearing as ADA61978, or treating a human patient suffering from
 CC infection caused by a bacteria comprising administering a mutant human
 XX

RESULT 7
 AAR10126 standard; protein; 124 AA.
 XX AC AAR10126;
 XX DT 25-MAR-2003 (revised)
 XX DT 19-MAR-1991 (first entry)
 DE Membrane-bound phospholipase A2 from human spleen.
 XX XX human phospholipase A2; anti-inflammatory drugs.
 XX XX Homo sapiens.
 XX XX JP02226081A.
 XX XX PD 26-NOV-1990.
 XX XX DR 27-APR-1989; 89JP-0011068.
 XX XX PN XX JP02226081A.
 XX XX PR 27-APR-1989; 89JP-0011068.
 XX XX PA (SHIO) SHIONOGI & CO LTD.
 XX XX DR WPI; 1991-012217/02.
 XX XX Human spleen deriving membrane bound phospholipase A2 - used for
 PT screening antiinflammatory drug.
 XX XX Claim 2; Page 1; 6pp; Japanese.

XX CC Human spleen was homogenized then centrifuged to obtain a precipitated
 CC pellet comprising the cell membrane component. The pellet was extracted
 CC with KBr ag. solution. Pure phospholipase A2 was obtained from the crude
 CC preparation by a combination of chromatography techniques. The protein

CC can be used as an antigen to generate monoclonal antibodies with CC specificity against human spleen-derived phospholipase A2. The CC monoclonal antibodies can be used in the diagnosis of inflammation. XX (Updated on 25-MAR-2003 to correct PA field.)

SQ Sequence 124 AA;

Query Match 49.9%; Score 360.5; DB 2; Length 124;
Best Local Similarity 55.6%; Pred. No. 1.4e-25;
Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;
XX

Qy 1 NLYQFGVMIEKMTGK-SALQYNDYGGCYCIGGSHWPDQTDKWCHAHDCYQRLEKJGE 59
Db 1 NLVNFHRMILKTICKERAAALSYGFVGCHGVGRGSPKDADTRCCVTHDCYRLEKRGCG 60
Qy 60 PKEKYLFLSERGLFCAGRTTCAKQDSCRSNSGSRTCAKODSCRSQKCECDKAATCPARNKTTYNKKYQYYSNKHCRGS 119
Qy 61 TKEFSYKFNSGSRTCAKODSCRSQKCECDKAATCPARNKTTYNKKYQYYSNKHCRGS 120
Qy 120 TPPC 123
Db 121 TPPC 124

RESULT 8

AAW73562 ID AAW73562 standard; protein; 124 AA.
XX AC AAW73562;

XX DT 10-MAR-1999 (first entry)

XX DE Human group II secretory phospholipase A2 protein.

XX Human group II secretory phospholipase A2; hsPLA2 grII; FXa inhibitor;

XX coagulation disorder; haemostatic disorder; FVa/FVa complex formation;

XX therapy.

XX Homo sapiens.

XX WO9855504-A1.

XX PR 10-DEC-1998.

XX (INSP) INST PASTEUR.

XX PF 04-JUN-1998; 98WO-IB0000869.

XX XX 05-JUN-1997; 97US-0048668P.

XX PA (INST) INST PASTEUR.

XX PI Mounier C, Hackeng T, Griffin J, Bon C;

XX DR 1999-045729/04.

XX New peptide fragment of human group II secretory phospholipase A2 (hsPLA2

XX grII) - useful in the treatment or prevention of coagulation and

XX hemostatic disorders.

XX PS Example 6; Page 27; 62pp; English.

XX This sequence represents the full length human group II secretory CC phospholipase A2 (hsPLA2 grII) protein. The invention relates to peptides CC comprising eleven amino acids, corresponding to residues 51-62 of 'hsPLA2 CC grII'. The peptides are useful in screening new compounds for their CC potential use as drugs in the treatment or prevention of coagulation CC disorders (particularly thrombus formation and limiting platelet CC activation in vivo in humans and animals). The peptides and antibodies CC form compositions in the regulation of the coagulant effect in vivo in CC humans or animals. The peptides are also useful, in forming kits in the CC detection of haemostatic disorders. Additionally, the peptides and CC antibodies form compositions in the treatment or prevention of CC haemostatic disorders. The peptide represents the specific region of CC hsPLA2 grII involved in the inhibition of the FVa/FVa complex formation,

CC and FXa inhibition, which maximizes the effects of drugs based on the CC peptide

XX SQ Sequence 124 AA;

Query Match 49.9%; Score 360.5; DB 2; Length 124;
Best Local Similarity 55.6%; Pred. No. 1.4e-25;
Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;
XX

Qy 1 NLVQFGVMIEKMTGK-SALQYNDYGGCYCIGGSHWPDQTDKWCHAHDCYQRLEKJGE 59
Db 1 NLVNFRMILKTICKERAAALSYGFVGCHGVGRGSPKDADTRCCVTHDCYRLEKRGCG 60
Qy 60 PKEKYLFLSERGLFCAGRTTCAKODSCRSQKCECDKAATCPARNKTTYNKKYQYYSNKHCRGS 119
Db 61 TKEFSYKFNSGSRTCAKODSCRSQKCECDKAATCPARNKTTYNKKYQYYSNKHCRGS 120
Qy 120 TPPC 123
Db 121 TPPC 124

RESULT 9

ADA61982 ID ADA61982 standard; protein; 124 AA.
XX AC ADA61982;

XX DT 20-Nov-2003 (first entry)

XX DE Human G72K PLA2 mutant.

XX KW Antibacterial; gram-positive bacteria; human; group IIA phospholipase A2;
KW group IIA PLA; bacterial infection; Staphylococcus aureus;
KW multi-drug resistance; wound; bloodstream infection;
KW methicillin-resistant S. aureus; MRSA; nosocomial infection;
KW vancomycin-resistant Enterococcus faecium; murein; mutant.

XX OS Synthetic.

OS Homo sapiens.

XX FH Key Location/Qualifiers
FT Misc-difference 72
FT /note= "Wild-type Gly substituted by Lys"

XX PN US6475484-B1.

XX PD 05-NOV-2002.

XX PP 18-DEC-2000; 2000US-00740569.

XX PR 17-DEC-1999; 99US-01724679.

XX PA (UTNY) UNIV NEW YORK STATE.

XX PI Weiss J, Elsbach P, Liang N;

XX DR WPI; 2003-219013/21.

XX PT Treating a patient suffering from infection caused by gram-positive PT bacteria or killing gram-positive bacteria, comprises delivering mutant PT human Group IIA phospholipase A2.

XX PS Example 1; Page 22pp; English.

XX The invention relates to killing gram-positive bacteria (I) in human CC patient, comprising contacting the bacteria with a bactericidal-effective CC amount of mutant human Group IIA phospholipase A2 (Group IIA PLA2). CC appearing as ADA61978, or treating a human patient suffering from CC infection caused by a bacteria comprising administering a mutant human CC Group IIA PLA2 and an antibiotic. The methods of the invention are useful CC for killing Gram-positive bacteria, (especially *Staphylococcus aureus*) CC and for treating human patient suffering from an infection caused by Gram CC

WPI; 2003-587105/55.

New fusion polypeptides, useful for immobilization or purification and isolation of the non-Tola polypeptide, or for studying interaction properties of the non-Tola polypeptide or the fusion polypeptide, e.g. self-interaction.

Example 1: Page 56-57; 68pp; English.

The present invention describes a fusion polypeptide (I) for expression in a host cell comprising a TolAII domain (functional homologue, fragment or derivative), and a non-Tola polypeptide, where the TolAII domain (functional homologue, fragment or derivative) is located towards the N-terminus of the fusion polypeptide, and the non-Tola polypeptide is located towards the C-terminus of the fusion polypeptide. Also described is (1) a DNA molecule (II) encoding the fusion polypeptide (I); (2) an expression vector (III) comprising (II) for expression of (I); (3) a cloning vector (IV) for producing the expression vector comprising DNA (II) encoding the TolAII domain (functional homologue, fragment or derivative) upstream or downstream from a cloning site which allows in-frame insertion of DNA encoding a non-Tola polypeptide, and (4) a host cell containing (II), and/or (III), and/or (IV). The TolAII domain (functional homologue, fragment or derivative) is useful for producing the fusion polypeptide (I), DNA molecule (II), expression vector (III) or cloning vector (IV). The fusion polypeptide (I) is useful for immobilisation or purification and isolation of the non-Tola polypeptide or for studying interaction properties of the non-Tola polypeptide or the fusion polypeptide, e.g. self-interaction, interaction with another molecule or interaction with a physical stimulus and for high expression of a polypeptide as a fusion polypeptide in a host cell. ACP57145 to ACP57146 and ABR8341 to ABR8374 represent sequences used in the exemplification of the present invention.

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Sequence 124 AA;
Query Match 49.9%; Score 360.5; DB 6; Length 124;
Best Local Similarity 55.6%; Pred. NO. 1.4e-25; Gaps
Matches 69; Conservative 9; Mismatches -45; Indexes 1;
Gaps 1

1 NLQFGVMILEKMTGK-SALQYNDPGCYYCGGSEMAPVDQTWCCCHAHDCCYGRLEKLGE 5
1 NLNFHRMQLTIGEKAALSYGFVGGCHCGGSSPKDADTRCCVTHDCCYKRLEKRGCG 6
60 PKEKYLPSVRSERGIFCAGRITCQLTCBODRALKCFRNLYGYNRKIAHYPNKLCTGP 1
61 TKFLSYKFNSGGSRITCAQDSRSQLCEDKRAAATCFARNKTHYNNKTYQQYSNKHCRGS 12
120 TPPC 123
121 TPRC 124

RESULT 12
AAP93112 AAP93112 standard; protein; 144 AA.
AAP93112;

25-MAR-2003 (revised)
31-JUL-1992 (first entry)

Human inflammatory phospholipase A2 encoded by HindIII fragment of PLA2
8.5 EMBL3.

Inflammation; acid stable; phosphatide 2-acetylhydrolase; lipolytic;
glycerophospholipids; non-pancreatic.

Homo sapiens.

Location/Qualifiers
Key 1
Peptide .20
Region /label= signal

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Db	81 TKFLSYKFSNSGSRITCAKQDSCRSQLECDKAATCFAARNKTYNCKYQQYSNKHCRGS	140	Db	81 TKFLSYKFSNSGSRITCAKQDSCRSQLECDKAATCFAARNKTYNCKYQQYSNKHCRGS	140
Qy	120 TPPC 123		Qy	120 TPPC 123	
Db	141 TPRC 144		Db	141 TPRC 144	
RESULT 13					
AAFP93363	standard; protein; 144 AA.				
ID	AAFP93363				
XX					
AC	AAFP93363_				
XX	25-MAR-2003 (revised)				
DT	27-JUN-1980 (first entry)				
XX	Human synovial phospholipase type A2 (sPLA2) as encoded by cDNA clone lambda sPLA2cDNA-4 and by the exons of clone lambda sPLA2-6 .				
DE					
DE	Human synovial phospholipase A2; clone lambda sPLA2cDNA-4 ;				
XX					
KW	Human synovial phospholipase A2; clone lambda sPLA2-6 .				
XX					
OS	Homo sapiens.				
XX					
FH	Key	Location/Qualifiers			
FT	Protein	21..144			
XX					
XX	WO8901773-A.				
PN					
XX	PD 09-MAR-1989.				
XX					
PF	23-AUG-1988;	88R0-US002896.			
XX					
PR	27-AUG-1987;	87US-00089883.			
PR	06-JUL-1988;	88US-00215726			
PR	-16-AUG-1988;	88US-00231865.			
XX					
PA	(BIOT-) BIOTECH RES PARTN. (UTOR) UNIV OF TORONTO INNOVAT.				
XX					
PI	Johnson JK, Seilhamer JJ, Pruzanski W, Vadas P;				
XX					
DR	1989-085394/11.				
DR	N-PSDB; ZAN91258, ZAN91260.				
XX					
PT	Mammalian synovial phospholipase A2 - used in food processing, design and screening of inflammation inhibitors, as an anticancer drug or vaccine adjuvant etc.				
PT					
PT	WPI: 1989-085394/11.				
XX					
CC	Clone lambda sPLA2cDNA-4 is one of four clones identified when probe oligo 2905 (ZAN91257) was used to screen a cDNA library constructed from polyA+ message from a peritoneal cell RNA. It encodes the entire sPLA2 type A sequence which is given here. The mature peptide sequence (see FT) has a calculated molecular weight of 13,919 daltons. The same amino acid sequence is also encoded by the exons of clone lambda sPLA2-6 (ZAN91260) in Figure 7. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)				
CC					
CC	Sequence 144 AA;				
CC	Score 360.5; DB 2; Length 144;				
CC	Best Local Similarity 55.6%; Pred. No. 1..6e-25;				
CC	Mismatches 9; Indels 45; Gaps 1;				
CC	Matches 69; Conservative 9; Gaps 1;				
CC	Indels 1; Gaps 1;				
XX					
Qy	1 NLVQFGWMIERMTGK-SALOQNNDYCGTGGCGTGGSHMPVDPQTDWCHAHDCYGRLEKLGCG	59	Qy	1 NLVQFGWMIERMTGK-SALOQNNDYCGTGGCGTGGSHMPVDPQTDWCHAHDCYGRLEKLGCG	59
Db	21 NLVNFRMIRKLTTGGEALYSYGFIGCHGGVGRSPKDAIDRCCTVTHCCYKLERKGCG	80	Db	21 NLVNFRMIRKLTTGGEALYSYGFIGCHGGVGRSPKDAIDRCCTVTHCCYKLERKGCG	80
Qy	60 PKELEYLFSVBERGIFCAVRTTCQRLTCECDKAATCFARNKTYNCKYQQYSNKHCRGS	119	Qy	60 PKELEYLFSVBERGIFCAVRTTCQRLTCECDKAATCFARNKTYNCKYQQYSNKHCRGS	119
Db	81 TKFLSYKFSNSGSRITCAKQDSCRSQLECDKAATCFARNKTYNCKYQQYSNKHCRGS	140	Db	81 TKFLSYKFSNSGSRITCAKQDSCRSQLECDKAATCFARNKTYNCKYQQYSNKHCRGS	140
Qy	1 NLVQFGWMIERMTGK-SALOQNNDYCGTGGCGTGGSHMPVDPQTDWCHAHDCYGRLEKLGCG	59	Qy	1 NLVQFGWMIERMTGK-SALOQNNDYCGTGGCGTGGSHMPVDPQTDWCHAHDCYGRLEKLGCG	59
Db	21 NLVNFRMIRKLTTGGEALYSYGFIGCHGGVGRSPKDAIDRCCTVTHCCYKLERKGCG	80	Db	21 NLVNFRMIRKLTTGGEALYSYGFIGCHGGVGRSPKDAIDRCCTVTHCCYKLERKGCG	80
Qy	60 PKELEYLFSVBERGIFCAVRTTCQRLTCECDKAATCFARNKTYNCKYQQYSNKHCRGS	119	Qy	60 PKELEYLFSVBERGIFCAVRTTCQRLTCECDKAATCFARNKTYNCKYQQYSNKHCRGS	119

RESULT 15
 AAR63055 standard; protein: 144 AA.
 XX
 AC AAR63055;
 XX
 DT 25-MAR-2003 (revised)
 DT 15-AUG-1995 (first entry)
 DE Human PLA2 type II.
 XX
 KW HPLA2-10; phospholipase A2; PLA2.
 XX
 OS Homo sapiens.
 XX
 PN WO95023328-A1.
 XX
 PD 26-JAN-1995.
 XX
 PF 15-JUL-1994; 94NO-US007926.
 XX
 PR 15-JUL-1993; 93US-00091941.
 PR 26-JUL-1993; 93US-00097354.
 XX
 (INDV) UNIV INDIANA FOUND.
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Tischfield JA, Seilhamer JJ;
 XX
 DR; 1995-067096/09.

XX
 PT Novel type III and IV low mol. wt. phospholipase A2 enzymes - from humans
 PT and rats, also nucleic acid sequences useful, e.g. for recombinant produc.
 PT of enzymes, research into Batten's disease, etc.
 PS Disclosure: FIG 15; 16QPP; English.

XX
 CC A human cDNA (AAQ01138) expressing a novel PLA2, HPLA2-10, was derived
 CC from human brain RNA by RACE-PCR. HPLA2-10 (AAR63046) was characterized
 CC as a novel type of PLA2, type IV, on the basis of its Cys content in
 CC comparison with human PLA2 types I (AAR63054) and II (AAR63055) (updated
 CC on 25-MAR-2003 to correct PN field.)
 XX

SQ Sequence 144 AA;

Query Match Score 360.5; DB 2; Length 144;
 Best Local Similarity 49.9%; Pred. No. 1.6e-25;
 Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;

Qy 1 NLVQFGVMIEKMTGK-SALQYNDYGCYGGIGGSHWPDQTDACCHAHDCCYCGRLEKLGCB 59
 Db 21 NLVNFHMRMKLTTREAAISYGFYGHCGGGGRGSPKDADRCCTVTHIDCCYCGRLEKRGCG 80
 Qy 60 PKEKYLFLFSYVSGRSIFCAERTTCORLTCEDRRAALCPRNLTYNKVAHYPNELCTGP 119
 Db 81 TKFLSYKPSNSGSRITCAKQDSCRSOLCEDXAAATCFARNKTYTNYKQYIYSNKHCRGS 140
 Qy 120 TPPC 123
 Db 141 TPRC 144

Search completed: July 3, 2004, 05:16:17
 Job time : 35.8113 secs



GenCore version 5.1.6
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I protein - protein search, using sw model

on: July 3, 2004, 05:17:51 ; Search time 43.6302 Seconds
(without alignments)
877.555 Million cell updates/sec

Title:	US-10-088-092A-30_COPY_20_142
Ref. score:	722
Sequence:	1 NLVQFGMIEKNTGKSALQY.....YNRKYAHYPNKLCTGPTPPC 123
oring table:	BLOSUM62
Gapext:	0.5
searched:	1276540 seqs, 31123816 residues
Total number of hits satisfying chosen parameters:	1276540
Minimum DB seq length: 0	
Maximum DB seq length: 2000000000	
st-processing: Minimum Match 0%	
Maximum Match 100%	
Listing first 45 summaries	
atabase :	Published Applications AA: 1: /cgm2_6/podata/2/pubpaas/007_PUBCOMB.pep: 2: /cgm2_6/podata/2/pubpaas/007_PCT_NEW_PUB.pep: 3: /cgm2_6/podata/2/pubpaas/006_NEW_PUB.pep: 4: /cgm2_6/podata/2/pubpaas/005_PUBCOMB.pep: 5: /cgm2_6/podata/2/pubpaas/005_PUBCOMB.pep: 6: /cgm2_6/podata/2/pubpaas/007_NEW_PUB.pep: 7: /cgm2_6/podata/2/pubpaas/008_PUBCOMB.pep: 8: /cgm2_6/podata/2/pubpaas/008_PUBCOMB.pep: 9: /cgm2_6/podata/2/pubpaas/009_PUBCOMB.pep: 10: /cgm2_6/podata/2/pubpaas/0095_PUBCOMB.pep: 11: /cgm2_6/podata/2/pubpaas/009_C_PUBCOMB.pep: 12: /cgm2_6/podata/2/pubpaas/009_NNEW_PUB.pep: 13: /cgm2_6/podata/2/pubpaas/010_PUBCOMB.pep: 14: /cgm2_6/podata/2/pubpaas/010B_PUBCOMB.pep: 15: /cgm2_6/podata/2/pubpaas/010C_PUBCOMB.pep: 16: /cgm2_6/podata/2/pubpaas/010_NNEW_PUB.pep: 17: /cgm2_6/podata/2/pubpaas/060_NNEW_PUB.pep: 18: /cgm2_6/podata/2/pubpaas/060_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	722	100.0	154	US-09-975-456B-8	Sequence 8, Appli
2	360.5	49.9	124	US-10-255-456B-2	Sequence 2, Appli
3	360.5	49.9	144	US-09-975-456B-6	Sequence 6, Appli
4	360.5	49.9	144	US-10-205-823-325	Sequence 325, App
5	360.5	49.9	144	US-10-115-275-269	Sequence 269, App
6	360.5	49.9	164	US-09-925-300-1010	Sequence 1010, Ap
7	341	47.2	146	US-09-993-999-8	Sequence 8, Appli
8	341	47.2	146	US-10-124-591-3	Sequence 3, Appli
9	337	46.7	146	US-10-124-591-4	Sequence 4, Appli
10	335.5	46.5	138	US-09-917-805-7	Sequence 7, Appli
11	330.5	45.8	138	US-09-917-805-6	Sequence 6, Appli
12	311.5	43.1	138	US-09-917-805-2	Sequence 2, Appli
13	303	42.0	168	US-09-975-456B-2	Sequence 2, Appli
14	303	42.0	168	US-10-104-373-3735	Sequence 3735, Ap
15	303	42.0	211	US-10-344-680-23	Sequence 23, Ann

Sequence 195, Appli
Sequence 2, Appli
Sequence 80, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 9, Appli
Sequence 17, Appli
Sequence 7, Appli
Sequence 6, Appli
Sequence 1342, Ap
Sequence 9, Appli
Sequence 10, Appli
Sequence 1, Appli
Sequence 511, App
Sequence 1, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 8, Appli
Sequence 5, Appli
Sequence 3, Appli
Sequence 511, App
Sequence 1, Appli
Sequence 7, Appli
Sequence 15, Appli
Sequence 10, Appli
Sequence 7, Appli
Sequence 10, Appli
Sequence 5548, AP
Sequence 378, APP
Sequence 534, APP
Sequence 534, APP

ALIGNMENTS

RESULT 1

; Sequence 8, Application US-C0975456B
; Publication No. US20030073087A1
; GENERAL INFORMATION:
; APPLICANT: LAJDUNSKI, MICHEL
; APPLICANT: LAMBEAU, GERARD
; APPLICANT: VALENTIN, EMANUEL
; TITLE OF INVENTION: NOVEL MAMMALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2
; FILE REFERENCE: 1478-R-00
; CURRENT APPLICATION NUMBER: US/09/975,456B
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/1239,491
; PRIOR FILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 2.1
; SEQ ID NO: 8
; LENGTH: 154
; TYPE: PPT
; ORGANISM: Homo sapiens
US-09-975-456B-8

Query Match 100 0%; Score 722; DB 10; Length 154;
Best Local Similarity 100 0%; Pred. No. 7e-71; Mismatches 0; Indels 0; Gaps 0;

Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 NLVQFGMIEKNTGKSALQNDYGCIGGSHWPQTDWCMCHADCCYGRLERKGCEP 60
2 NLVQFGMIEKNTGKSALQNDYGCIGGSHWPQTDWCMCHADCCYGRLERKGCEP 91
3 KLEKYLFSVERGIFCAAGRITCQRLTCEDKRAILCFRRNLGTYNRKYAHYPNKLCTGPT 120
4 KLEKYLFSVERGIFCAAGRITCQRLTCEDKRAILCFRRNLGTYNRKYAHYPNKLCTGPT 151

RESULT 2
US-10-255-576-2
Sequence 2, Application US/10255576
Publication No. US20030161822A1
GENERAL INFORMATION:
APPLICANT: Weiss, Jerryold
APPLICANT: Elsbach, Peter
APPLICANT: Liang, Ning-Sheng
TITLE OF INVENTION: ANTI-BACTERIAL GROUP IIA PHOSPHOLIPASE A2 AND METHODS OF USE THERE
FILE REFERENCE: 598611E917US1
CURRENT APPLICATION NUMBER: US/10/255,576
CURRENT FILING DATE: 2002-09-15
PRIOR APPLICATION NUMBER: US/09/740,569
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US 60/172,467
PRIOR FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 2
LENGTH: 124
TYPE: PRT
ORGANISM: Homo sapiens
US-10-255-576-2

Query Match 49.9%; Score 360.5; DB 14; Length 124;
Best Local Similarity 54.8%; Pred. No. 5.8e-32;
Matches 68; Conservative 11; Indels 1; Gaps 1;

Qy 1 NLVQFVMIERMTGK-SALOQNNDYCGCIGGSHWPVDOTDWCCHAHDCCYGRBLEKGCG 59
Db * 1 NLVNFRHLKLTGKTYTSGYFGCHCGGRGSXDAIDRCCYTHCCYKRLEKGCG 60

Qy 60 PKEKYLFSYSERGIFCAERTTCQRLTCBDRKAALCPFRNLGTYNRKAYHNKLCTGP 119
Db 61 TRPLSYKFNSKSRSRITCAKQDSCRSQLCECDKAAATCPARNKTYTNKQYISNKHCRGS 120

Qy 120 TPPC 123
Db 121 TPPC 124

RESULT 3
US-09-975-4563-6
Sequence 6, Application US/09973456B
Publication No. US2003073087A1
GENERAL INFORMATION:
APPLICANT: LAZDINSKI, MICHEL
APPLICANT: LAMBEAU, GERARD
APPLICANT: VALENTIN, EMMANUEL SECRETED GROUP IIF PHOSPHOLIPASE A2
FILE REFERENCE: 1474-R-00
CURRENT APPLICATION NUMBER: US/09/975,456B
CURRENT FILING DATE: 2002-08-27
PRIOR APPLICATION NUMBER: 60/239,491
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 2.1
SEQ ID NO: 6
LENGTH: 144
TYPE: PRT
ORGANISM: Homo sapiens
US-09-975-4563-6

Query Match 49.9%; Score 360.5; DB 10; Length 144;
Best Local Similarity 55.6%; Pred. No. 6.8e-32;
Matches 9; Conservative 45; Indels 1; Gaps 1;

Qy 1 NLVQFVMIERMTGK-SALOQNNDYCGCIGGSHWPVDOTDWCCHAHDCCYGRBLEKGCG 59
Db 21 NLVNFRHLKLTGKTYTSGYFGCHCGGRGSXDAIDRCCVTHDCCYKRLEKGCG 80

Qy 60 PKEKYLFSYSERGIFCAERTTCQRLTCBDRKAALCPFRNLGTYNRKAYHNKLCTGP 119
Db 81 TRPLSYKFNSKSRSRITCAKQDSCRSQLCECDKAAATCPARNKTYTNKQYISNKHCRGS 140

Qy 120 TPPC 123
Db 121 TPPC 144

RESULT 4
US-10-205-823-325
Sequence 325, Application US/10205823
Publication No. US20030108963A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Endege, Wilson O.
APPLICANT: Gannav Narapu, Manjula
APPLICANT: Gorbatcheva, Bella
APPLICANT: Hoersch, Sebastian
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Wonsley, Angela M.
APPLICANT: Zhao, Xumei
APPLICANT: Anderson, Dustin
APPLICANT: Glatt, Karen
APPLICANT: Xumei
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND PREVENTION, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF PROSTATE CANCER
CURRENT APPLICATION NUMBER: US/10/205,823
CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/307,982
PRIOR FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: 60/314,356
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/335,020
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/362,158
PRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 325
LENGTH: 144
TYPE: PRT
ORGANISM: Homo sapiens
US-10-205-823-325

Query Match 49.9%; Score 360.5; DB 14; Length 144;
Best Local Similarity 55.6%; Pred. No. 6.8e-32;
Matches 9; Mismatches 45; Indels 1; Gaps 1;

Qy 1 NLVQFVMIERMTGK-SALOQNNDYCGCIGGSHWPVDOTDWCCHAHDCCYGRBLEKGCG 59
Db 21 NLVNFRHLKLTGKTYTSGYFGCHCGGRGSXDAIDRCCVTHDCCYKRLEKGCG 80

Qy 60 PKEKYLFSYSERGIFCAERTTCQRLTCBDRKAALCPFRNLGTYNRKAYHNKLCTGP 119
Db 81 TRPLSYKFNSKSRSRITCAKQDSCRSQLCECDKAAATCPARNKTYTNKQYISNKHCRGS 140

Qy 120 TPPC 123
Db 121 TPPC 144

RESULT 5
US-10-116-275-269
Sequence 269, Application US/10116275
Publication No. US20030211476A1
GENERAL INFORMATION:
APPLICANT: Elan Pharmaceutical Technology
APPLICANT: O'Mahony, Daniel J.
APPLICANT: Brayden, David

Qy 1 NLVQFVMIERMTGK-SALOQNNDYCGCIGGSHWPVDOTDWCCHAHDCCYGRBLEKGCG 59
Db 21 NLVNFRHLKLTGKTYTSGYFGCHCGGRGSXDAIDRCCVTHDCCYKRLEKGCG 80

Qy 60 PKEKYLFSYSERGIFCAERTTCQRLTCBDRKAALCPFRNLGTYNRKAYHNKLCTGP 119

RESULT 7
 US-09-993-999-8
 ; Sequence 8, Application US/09993999
 ; Patent No. US20020110891A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ho, I-Cheng
 ; ADDRESS: Arm, Jonathan P.
 ; APPLICANT: Austen, K. Frank
 ; APPLICANT: Glimcher, Laurie H.
 ; TITLE OF INVENTION: Phospholipase A2 Group Preferentially
 ; EXPRESSED in The Cells
 ; FILE REFERENCE: HUI-06
 ; CURRENT APPLICATION NUMBER: US/09/993,999
 ; CURRENT FILING DATE: 2001-11-06
 ; PRIOR APPLICATION NUMBER: 60/246,316
 ; PRIORITY DATE: 2000-11-06
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 8
 ; LENGTH: 144
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-116-275-269

Query Match Score 360.5; DB 15; Length 144;
 Best Local Similarity 55.6%; Pred. No. 6.8e-32;
 Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;

Qy 1 NLVQFGVMIEKMTGK-SALQYNDYGYCGIGGSWHPDQTDWCCCHAHDCCYGRLEKGCG 59
 Db 21 NLVNFRHMRMLTKEALSYGFYGCCHCQVGRGSQPKDATDRCCVTHDCYKRLEKGCG 80

Query Match Score 341; DB 9; Length 146;
 Best Local Similarity 52.8%; Pred. No. 9.9e-30;
 Matches 66; Conservative 48; Mismatches 49; Indels 2; Gaps 2;
 Qy 1 NLVQFGVMIEKMTGKSA-LOYNDYGYCGIGGSWHPDQTDWCCCHAHDCCYGRLEKGCG 59
 Db 22 NTAQFEMIRLTKGRKELSYAFYGCCHCQVGRGSQPKDATDRCCVTHDCYKRLEKGCG 81

Qy 60 PKLEYKLFYSVERGIFCAERTTCORLTCEDKRAALCPRNLGTYNRKYAHYPNKLCTGP 119
 Db 81 TKEFLSYKFNSGSRTCAKQDSCRSOLCECDKAATCPARNKTTYNKQYIYSNKHCRGS 140

Qy 120 TPPC 123
 Db 141 TPPC 144

RESULT 6
 US-09-925-300-1010
 ; Sequence 1010, Application US/09925300
 ; Patent No. US20020151681A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Craig Rosen,
 ; ADDRESS: Steve Rubin,
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PA101
 ; CURRENT APPLICATION NUMBER: US/09/925,300
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05988
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 1880
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 1010
 ; LENGTH: 164
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-925-300-1010

Query Match Score 360.5; DB 9; Length 164;
 Best Local Similarity 55.6%; Pred. No. 7.8e-32;
 Matches 69; Conservative 45; Indels 1; Gaps 1;

Qy 1 NLVQFGVMIEKMTGK-SALQYNDYGYCGIGGSWHPDQTDWCCCHAHDCCYGRLEKGCG 59
 Db 41 NLVNFRHMRMLTKEALSYGFYGCCHCQVGRGSQPKDATDRCCVTHDCYKRLEKGCG 100

Qy 60 PKLEYKLFYSVERGIFCAERTTCORLTCEDKRAALCPRNLGTYNRKYAHYPNKLCTGP 119
 Db 101 TKEFLSYKFNSGSRTCAKQDSCRSOLCECDKAATCPARNKTTYNKQYIYSNKHCRGS 160

Qy 120 TPPC 123
 Db 161 TPPC 164

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0403 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555
 TELEFAX: 650-845-4166
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 146 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GenBank
 CLONE: 984837

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-124-591-3

Query Match 47.2%; Score 341; DB 13; Length 146;
 Best Local Similarity 52.8%; Pred. No. 9.9e-30;
 Matches 66; Conservative 9; Mismatches 48; Indels 2; Gaps 2;

Qy 1 NLVQFGVMIEKMTGKSA-IQNDYGCYCGIGSHMPVQTDWCHAHDCGYGRLEKLGCE 59
 Db 22 NIAQGEMMLRKTGKRAELSYAFQCHGUGGGSPKDATDRCVTHDCCKSLEKSGCG 81

Qy 60 PKLEYLFSYSERGIFCA-AGRITCQLRTCECDKRAALCFRRNLTGYNRKYAHYPNKLCTG 118
 Db 82 TRLLKTKYISHQGGQTCSANQNSCOKRLQCDKAAECFARNKKTSLKYQFYPNMFCKG 141

Qy * 119 TPPPC 123
 Db 142 RKP KC 146

RESULT 9
 Sequence 4, Application US/10124591
 Publication No. US20040177208A1
 GENERAL INFORMATION:
 APPLICANT: Hawkins, Phillip R.
 Bandman, Olga
 Guegler, Karl J.
 Shah, Purvi
 Corey, Neil C.

TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN

NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Dr.
 CITY: Palo Alto
 STATE: CA
 ZIP: 94304

COMPUTER READABLE FORM:
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/124,591
 FILING DATE: 16 Apr 2002
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/489,770
 FILING DATE: <Unknown>
 APPLICATION NUMBER: 08/966,317
 FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0403 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555
 TELEFAX: 650-845-4166
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 146 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GenBank
 CLONE: 204319

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-124-591-4

Query Match 46.7%; Score 337; DB 13; Length 146;
 Best Local Similarity 50.4%; Pred. No. 2.8e-29;
 Matches 63; Conservative 14; Mismatches 46; Indels 2; Gaps 2;

Qy 1 NLVQFGVMIEKMTGKSA-IQNDYGCYCGIGSHMPVQTDWCHAHDCGYGRLEKLGCE 59
 Db 22 SLLEQGMILFKTGKADVSFGFVHCCYNRLEKRGCG 81

Qy 60 PKLEYLFSYSERGIFCA-AGRITCQLRTCECDKRAALCFRRNLTGYNRKYAHYPNKLCTG 118
 Db 82 TKFLTYKFSTRGQQISCTMDSCRKQLOQCDKAAECFARNKKTSLKYQFYLINKFCKG 141

Qy 119 TPPPC 123
 Db 142 KTPSC 146

RESULT 10
 US-09-917-805-7
 Sequence 7, Application US/09917805
 Publication No. US20040073973A1
 GENERAL INFORMATION:
 APPLICANT: STYME, Sten
 APPLICANT: STAHL, Ulf
 APPLICANT: BK, Bo
 APPLICANT: SJODAHL, Staffan
 FILE REFERENCE: STYME=1
 CURRENT APPLICATION NUMBER: US/09/917,805
 CURRENT FILING DATE: 2001-07-31
 PRIOR APPLICATION NUMBER: 09/15,124
 PRIOR FILING DATE: 1999-03-02
 PRIOR APPLICATION NUMBER: PCT/SE97/00554
 PRIOR FILING DATE: 1997-03-27
 PRIOR APPLICATION NUMBER: 9601237.2
 PRIOR FILING DATE: 1996-03-29
 NUMBER OF SEQ ID NCS: 14
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 7

TYPE: PRT
 ORGANISM: Bothrops jararacussu

US-09-917-805-7

Query Match 46.5%; Score 335.5; DB 12; Length 138;
 Best Local Similarity 50.0%; Pred. No. 3.8e-29;
 Matches 62; Conservative 12; Mismatches 47; Indels 3; Gaps 2;

Qy 1 NLVQFGVMIEKMTGKSA-IQNDYGCYCGIGSHMPVQTDWCHAHDCGYGRLEKLGCE 59
 Db 17 DLWQFGMILKETGKLPFPYTTGCGGGGGGGPKDAIDRCCFVHDCCYGLKGLGE 74

Qy 60 PKLEYLFSYSERGIFCA-AGRITCQLRTCECDKRAALCFRRNLTGYNRKYAHYPNKLCTG 119
 Db 75 PKDTRYSRENGVIICTGGTPCEQICEDKAARAVFRENLYKMRMAYPDVLCKP 134

Qy 120 TPPC 123
 Db 135 AEKC 138

RESULT 11

; Sequence 6, Application US/09917805
; Publication No. US20040073973A1
; GENERAL INFORMATION:
; APPLICANT: STYNE, Sten
; APPLICANT: STAHL, Ulf
; APPLICANT: EK, Bo
; APPLICANT: SJODAHL, Staffan
; TITLE OF INVENTION: PLANT ENZYME AND USE THEREOF
; CURRENT APPLICATION NUMBER: US/09/917,805
; CURRENT FILING DATE: 2001-07-31
; PRIORITY NUMBER: 09/155,124
; PRIOR APPLICATION NUMBER: PCT/SE97/00554
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: 9601237.2
; PRIOR FILING DATE: 1996-03-29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Vipera ammodytes
; US-09-917-805-6

Query Match 43.1%; Score 311.5; DB 12; Length 138;
Best Local Similarity 50.8%; Pred. No. 1.7e-26;
Matches 63; Conservative 12; Mismatches 44; Indels 5; Gaps 4;

Qy 2 LVQFGVMIEKMTGKSA-LQYNDGCYCGIGGSHWVQDQTDWCCHAHDCCYGRLEKLGCE 60
Db 18 LWQFEMMIKVKKSGILSYASYYCGWNGRGPDKDATDRCCFVHDCCYGV -TGCPN 75

Qy 61 KLEKTYLFSVSRGIFGAGRTICQRLTECDKRAALCFERNLGTYNR-KYAHYPNLCTGP 119
Db 76 KLKGKTYTSWNGDIVCEGDPCKEV-CECDRAAAICFRDNLDYDRNKTYWRYPASNCQED 134

Qy 120 TPPC 123
Db 135 SBPC 138

RESULT 13

; Sequence 2, Application US/09975456B
; Publication No. US20030073087A1
; GENERAL INFORMATION:
; APPLICANT: LAZDUNSKI, MICHEL
; APPLICANT: LAMBEAU, GERARD
; APPLICANT: VALENTIN, EMMANUEL
; TITLE OF INVENTION: NOVEL MAMMALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2
; FILE REFERENCE: 1478-R-00
; CURRENT APPLICATION NUMBER: US/09/975,456B
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/239,491
; PRIOR FILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 2.1
; SEQ ID NO 2
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-975-456B-2

Query Match 42.0%; Score 303; DB 10; Length 168;
Best Local Similarity 43.3%; Pred. No. 1.9e-25;
Matches 55; Conservative 18; Mismatches 48; Indels 6; Gaps 4;

Qy 1 NLVQFEMIEKMTGKSA-LQYNDGCYCGIGGSHWVQDQTDWCCHAHDCCYGRLEKLGCE 59
Db 17 SLLEFGMMLGETCKNPVPSYSPYCYGGGGTPKDATDRCCFVHDCCYGNLP--DCS 74

Qy 60 PKEKYLFSVSRGIFGAGRTICQRLTECDKRAALCFERNLGTYNRKYAHYPNLCTGP 119
Db 75 PKCDRYKVRENNAAIVCGKGTSCENRICECDRAAAICFRKNLKTANYYRPDFLKKE 134

Qy 120 TPPC 123
Db 135 SEKC 138

RESULT 12

; Sequence 2, Application US/09917805
; Publication No. US20040073973A1
; GENERAL INFORMATION:
; APPLICANT: STYNE, Sten
; APPLICANT: STAHL, Ulf
; APPLICANT: EK, Bo
; TITLE OF INVENTION: PLANT ENZYME AND USE THEREOF
; CURRENT APPLICATION NUMBER: US/09/917,805
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 09/155,124
; PRIOR FILING DATE: 1997-03-02
; PRIOR APPLICATION NUMBER: PCT/SE97/00554
; PRIOR APPLICATION NUMBER: 9601237.2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Trimeresurus flavoviridis
; US-09-917-805-2

Qy 1 NLVQFEMIEKMTGKSA-LQYNDGCYCGIGGSHWVQDQTDWCCHAHDCCYGRLEKLGCE 60
Db 21 SLLNLKAMVEAVGTSATISVGCGCGRGPDKDVEWDWCCHAHDCCYQEFQDGCH 80

Qy 60 PKEKYLFSV-SERGIFCA-GRTQQLTCEDKRAALCFERNLGTYNRKYAHYPNLCTGP 116
Db 81 PYVDHYDHTIENNTEVCSDLNKTEDKQTMCMDKMNVLCLMQ -TYREERYGFLNYTC 138

Qy 117 TGPTPPC 123
Db 139 QGPTPNC 145

RESULT 14

; Sequence 3735, Application US/10104047
; Publication No. US20030236592A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236352A1 full length cDNA
; FILE REFERENCE: HI-A1015
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3735
; LENGTH: 168
; TYPE: PRT

Organism: Homo sapiens
US-10-047-3735

Query Match 42.0%; Score 303; DB 15; Length 168;
Best Local Similarity 43.3%; Pred. No. 1; e-25;
Matches 55; Conservative 18; Mismatches 48; Indels 6; Gaps 4;

Search completed: July 3, 2004, 05:27:05
Job time : 43.6302 secs

Qy 1 NLVQFGVMTKGRKSA-LQYNDGCGYGGSHWPVDQTDWCHAHDCCYGRLEKGCE 59
Db 21 SLLNLKAMVEAVTGRSAILISFVGCGCYCLGRGQPKDEVDWCHAHDCCYOBLFDGCH 80

Qy 60 PKLEYLFSV-SERGIFCA-GRTTCQRLTCECDKRAALCFRNLGTYNRYAHYNKLC 116
Db 81 PYVDHYDHTENNTTEIVCSDLNKTECDKROTMCDBRNMYCLMNO-TYREYRGFLNVYC 138

Qy 117 TGPTPPC 123
Db 139 QGPTPNC 145

RESULT 15
US-10-345-680-23

Sequence 23, Application US/10345680
Publication No. US20030148394A1

GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Silios-Santiago, Immaculada
APPLICANT: Venkateswarlu, Karichetti

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
TITLE OF INVENTION: 641, 260, 55089, 21407, 42012, 46656, 62555, 302, 323,
TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
TITLE REFERENCE: WPI02-012PRNM, OMNI

CURRENT APPLICATION NUMBER: US/10/345,680
CURRENT FILING DATE: 2003-01-16
PRIOR APPLICATION NUMBER: US 60/349,511
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/360,500
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/365,041
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 60/374,063
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/403,468
PRIOR FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: US 60/414,262
PRIOR FILING DATE: 2002-09-27
PRIOR APPLICATION NUMBER: US 60/419,986
PRIOR FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: US 60/423,809
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: US 60/429,797
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 66
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 211
TYPE: PRT
ORGANISM: Homo Sapiens

Query Match 42.0%; Score 303; DB 14; Length 211;
Best Local Similarity 43.3%; Pred. No. 2; e-25;
Matches 55; Conservative 18; Mismatches 48; Indels 6; Gaps 4;

Qy 1 NLVQFGVMTKGRKSA-LQYNDGCGYGGSHWPVDQTDWCHAHDCCYGRLEKGCE 59
Db 64 SLLNLKAMVEAVTGRSAILISFVGCGCYCLGRGQPKDEVDWCHAHDCCYOBLFDGCH 123

Qy 60 PKLEYLFSV-SERGIFCA-GRTTCQRLTCECDKRAALCFRNLGTYNRYAHYNKLC 116
Db 124 PYVDHYDHTENNTTEIVCSDLNKTECDKROTMCDBRNMYCLMNO-TYREYRGFLNVYC 181

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OM protein - protein search, using sw model

Run on: July 3, 2004, 05:13:08 ; Search time 25.9925 Seconds

(without alignments)

1493.077 Million cell updates/sec

Title: US-10-088-092A-30_COPY_20_142

Perfect score: 722

Sequence: 1 NLVQFGWMIEKNTGKSALQY..... YNRKYAHYPNKLCTGFTPPC 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 101/041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTRIMBL 25:*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rrodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriophage:*

17: sp_archaea:*

Q7t2r1	vipera russ
Q800c3	crotalus vi
Q8ce14	mus musculus
Q7t3t5	vipera russ
Qbn435	homo sapien
Q7zzq1	vipera russ
Q73s7	echis carin
Q8o4d7	bothrops ja
Q8k0y1	mus musculus
Q8bj93	mus musculus
Q7t1c6	vipera aspi
Q8c5y6	mus musculus
Q9qx68	mesocricetus auratus
Q8ay48	bungarus caeruleus
Q8axw0	bungarus muelleri
Q8axw1	bungarus muelleri
Q7tiro	bungarus fischeri
Q7zw60	rana catesbeiana
Q8axw2	bungarus muelleri
Q7t1rl	bungarus fischeri
Q9debo	pugnus major
Q8axw7	micruroides eurydice
Q8ws88	adamsia carinifera
Q7t2q4	bungarus fischeri
Q80211	latastea latastei
Q9t8p8	asterina pectinifera
Q7t2q5	bungarus fischeri
Q9yhn2	dientrachus guttatus
Q9u8p9	asterina pectinifera

ALIGNMENTS

RESULT 1

091y34	ID	091y34	PRELIMINARY;	PRT;	146 AA.
	AC	091y34;			
	DT	01-DEC-2001	(TREMBL)1.19, Created)		
	DT	01-DEC-2001	(TREMBL)1.19, Last sequence update)		
	DT	01-OCT-2003	(TREMBL)1.25, Last annotation update)		
	DE	Platelet phospholipase A2 precursor (Fragment).			
	OS	Battus norvegicus (Rat)			
	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheroidea; Rodentia; Muridae; Sciurognathi; Murinae; Rattus.			
	OX	NCBI_TaxID=10116;			
	RN	[1]			
	RP	SEQUENCE FROM N.A.			
	RC	STRAIN=Nistar; TISSUE=Blood;			
	RA	Liu T.T., Liang N.S., Meng Z.Q., Xie Y.A., Kuang Z.P., Li Y.; Cloning and sequence determination of rat platelet phospholipase A2 from whole blood.";			
	RT	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.			
	RL	EMBL; AF365363; AAK52061.1/-; DR GO; GO:0005509; F:calcium ion binding; IEA.			
	DR	DR GO; GO:0004623; F:phospholipase A2 activity; IEA.			
	DR	DR InterPro; IPR012111; Phospholipase2.			
	DR	DR PFAM; PF00068; phospholipase1.			
	DR	DR PRINTS; PRO0389; PHOSPHOLIPASE2.			
	DR	DR ProDom; PDD00303; PhospholipaseA2.			
	DR	DR SMART; SM00085; PA2C; 1.			
	DR	DR PROSITE; PS000119; PA2_ASF; 1.			
	DR	DR PROSITE; PS000118; PA2_His; 1.			
	KW	Signal.			
	FT	FT SIGNAL.			
	FT	FT CHAIN.	1	21	POTENTIAL.
	FT	FT TER.	22	>146	PLATELET PHOSPHOLIPASE A2.
	FT	FT SEQUENCE.	146	146	MW; 601C9EC85DCBD67 CRC64;
	FT	FT	146 AA;	146	Query Match Score 349.3%; Length 146;
	FT	FT	Best Local Similarity 51.2%; Pred. No. 3..LE 11..	2	Best Local Similarity 51.2%; Pred. No. 3..LE 11..
	FT	FT	Matches 64; Conservative 14; Mismatches 45; Indels 2; Gaps 2;		Matches 64; Conservative 14; Mismatches 45; Indels 2; Gaps 2;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	349	48.3	146	11 Q91y34	Q91y34 rattus norvegicus
2	335.5	46.2	138	13 Q7t1d5	Q7t1d5 vipera berus
3	325.5	45.1	138	13 Q805a3	Q805a3 trimeresurus
4	323.5	44.8	138	13 Q8ay1	Q8ay1 bothrops jaegeri
5	323.5	44.8	138	13 Q805a2	Q805a2 trimeresurus
6	315.5	43.7	138	13 Q7zta8	Q7zta8 crotalus viridis
7	314.5	43.6	138	13 Q7zta6	Q7zta6 crotalus viridis
8	313.5	43.4	138	13 Q7t1d1	Q7t1d1 vipera berus
9	312.5	43.3	138	13 Q7t1d4	Q7t1d4 vipera aspis
10	312.5	43.3	138	13 Q7t1d3	Q7t1d3 vipera aspis
11	312.5	43.3	138	13 Q7t1d2	Q7t1d2 vipera aspis
12	310.5	43.0	138	13 Q800c1	Q800c1 crotalus viridis
13	309.5	42.9	138	13 Q800c2	Q800c2 crotalus viridis
14	309.5	42.9	138	13 Q7zta7	Q7zta7 crotalus viridis
15	305.5	42.3	138	13 Q800c4	Q800c4 crotalus viridis
16	303	42.0	168	4 Q8n217	Q8n217 homo sapiens

Qy	1 NLVQFGVMTKGSAA-LQYNDYGCYCGIGGSHWPIDQTDMCCHADCCGCRLEKGCE	RA Chiiwa T., Hamai S., Tsubouchi S., Ogawa T., Deshimaru M.,
Dy	22 SLLERGQMFPEKTKRADYSGFVGCHGVGGSPXDAIDNCCTVHDCCNRLERKGCG	RA Oda-Ueda N., Hattori S., Kubara H., Tsunazawa S., Ohno M.,
Db	60 PKLXEYLFSYERGIFCA-GRTTQLRLETCDFDRAALCFRNLGTYNRKAHYPNKLCTG	RT "Intricisland mutation of a novel phospholipase A2 from Trimeresurus flavoviridis venom and evolution of crotalinae group II phospholipase A2."
Qy	82 TKFLTYKFSYRGGRISCTNQDSCKQLCQCDKAEECFARNKKSYLKYQFYPNKECKG	RT Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
Dy	119 PTPPC 123	DR EMBL; AB102728; BA56892.1;
Qy	142 KTPSC 146	DR GO; GO:0005509; F:calcium ion binding; IEA.
Db		DR GO; GO:0004623; F:phospholipase A2 activity; IBA.
RESULT 2		DR GO; GO:0016042; F:Lipid catabolism; IBA.
QTT1DS	PRELIMINARY;	DR InterPro; IPR001211; PhospholipaseA2.
ID	PRT; 138 AA.	DR Pfam; PF00068; Phoslip; 1.
AC		DR PRINTS; PRO0389; PHOSPHOLIPASEA2; 1.
DT	01-OCT-2003 (TREMBLrel. 25, Created)	DR PRODOM; PD000303; PAAC; 1.
DT	01-OCT-2003 (TREMBLrel. 25, Last sequence update)	DR SMART; SM00085; PAAC; 1.
DB	Phospholipase A2.	DR PROSITE; PS000119; PA2 ASP; 1.
GN	PLA2VB.	DR PROSLICE; PS000118; PA2_HIS; 1.
OS	vipera berus (Common viper), Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Lepidosaurs; Squamata; Scleroglossa; Serpentes; Colubroidea; OC Viperidae; Viperinae; Vipera.	DR SEQUENCE; 138 AA; 15817 MN; 1;
NCBI_TAXID	[1] -	
RN	SEQUENCE FROM N.A.	
RX	MEDLINE=22707820; PubMed=12823540;	DR 120 TPPC 123
RA	"Guillemin J., Bouchier C., Garrigues T., Wisner A., Choumet V., "Sequences and structural organization of phospholipase A2 genes from Vipera aspis aspis V. aspis zinnikeri and Vipera berus berus venom. RT Identification of the origin of a new viper population based on RT ammodytin II heterogeneity."	DR 135 TEKC 138
RL	Eur. J. Biochem. 269:2709-2706(2003).	
DR	EMBL; AY18636; AAN59982.1; -.	
SQ	SEQUENCE 138 AA; 15716 MW; 79B9F9E0D16C9CCB CRC64;	
Qy	1 NLVQFGVMTKGSAA-QYNDYGCYCGIGGSHWPIDQTDMCCHADCCGCRLEKGCE	RESULT 4 OXYXYI PRELIMINARY; PRT; 138 AA.
Dy	46-2%; Score 333 5; DB 13; Length 138;	TD Q8AXYI; PRELIMINARY;
DT	Best Local Similarity 48.4%; Pred. No. 2e-31; Indels 3; Gaps 2;	AC ACQAXYI; PRELIMINARY;
DB	Matches 60; Conservative 14; Mismatches 47; Indels 3; Gaps 2;	DT DT01-MAR-2003 (TREMBLrel. 23, Created)
Qy	17 NLFOGFMNMINHMGKHAWSYLSYCYGGCGKGRPAQDTRCCFVHDCCYGRAN- -GCD	DT DT01-MAR-2003 (TREMBLrel. 23, Last sequence update)
Dy	60 PKLXEYLFSYERGIFCA-GRTTQLRLETCDFDRAALCFRNLGTYNRKAHYPNKLCTG	DT DT01-OCT-2003 (TREMBLrel. 25, Last annotation update)
Db	75 PKSDIYSYSWKTGKVIIIGEGTECEKQICBECQDRAAVCFSONLRTYKXKYMFYBDFLCCTDP	DE Hypotensive phospholipase A2.
Qy	75 PKLXEYLFSYERGIFCA-GRTTQLRLETCDFDRAALCFRNLGTYNRKAHYPNKLCTG	OS Bothrops jararacussu (Jararacussu).
Dy	120 TPPC 123	OC Eukaryota; Metzoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Db	135 SDKC 138	OC Lepidosaurs; Squamata; Scleroglossa; Serpentes; Colubroidea;
Qy	120 TPPC 123	OC Viperidae; Crotalinae; Bothrops.
Dy	135 SDKC 138	OX NCBI_TAXID=8726; 1;
RESULT 3		RN SEQUENCE FROM N.A.
Q805A3	PRELIMINARY;	RC TISSUE-Venom Gland; MEDLINE=22157211; PubMed=12167491;
ID	PRT; 138 AA.	RC SEQUENCE FROM N.A.
AC	Q805A3;	RC TISSUE-Venom Gland; Andriolo-Escaro S.H., Soares A.M., Fontes M.R., Fuly A.L.,
DT	01-JUN-2003 (T-TREMBLrel. 24, Created)	RC Roberto P.G., Kashima S., Soares A.M., Astolfi-Filho S., Giglio J.R.,
DT	01-JUN-2003 (T-TREMBLrel. 24, Last sequence update)	RC Franca S.C.;
DB	Phospholipase A2.	RC "Functional and structural analysis of Acidic and Basic Phospholipases A2 from Bothrops jararacussu Snake Venom."
GN	PLA-N.	RT Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
OS	Trimeresurus flavoviridis (Habu).	DR EMBL; AY145336; DR GO; GO:0005509; F:calcium ion binding; IEA.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	DR GO; GO:0004623; F:phospholipase A2 activity; IBA.
OC	Viperidae; Crotalinae; Trimeresurus.	DR GO; GO:0016042; F:Lipid catabolism; IBA.
OX		DR InterPro; IPR001211; PhospholipaseA2.
RN	SEQUENCE FROM N.A.	DR Pfam; PF00068; phoslip; 1.
RP		

DR	PR00389; PHPLIPASEA2.						
DR	ProDom; PD000303; PhospholipaseA2; 1.						
DR	SMART; SM00085; PA2c; 1.						
DR	PROSITE; PS00119; PA2 ASP; 1.						
DR	PROSITE; PS00118; PA2 HIS; 1.						
SQ	SEQUENCE 138 AA; 15456 MW;	513647907BFDD0F4E CRC64;					
Query Match	44.8%; Score 323.5; DB 13; Length 138;						
Best Local Similarity	46.8%; Pred. No. 3e-30;						
Matches	58; Conservative 16; Mismatches 47; Indels 3; Gaps 2;						
QY	1 NLVQFGVMIEKMTGKS-AIQLQNDYCYCIGGSHWPVDQTDWCCAHADCCYGRLEKLGC 59						
Db	17 SLWQFERMINTVMGEGLVQFLQSYGCGGGQOPTDAEDRCCFVHDCCYGRV-TGCD 74						
QY	60 PKEKYLPSVSERGFCAGRITCQLLTCEDKRAALCFRNLGYTARKTAHYPAKLCGP 119						
Db	75 PKIDSYTSKXNGDVGDDPCKRQICEDRVATTCPFDNKDITYDIKYWFYGRKNQCEK 134						
Qy	120 TPPC 123						
Db	135 SEPC 138						
RESULT 5							
Q80582	PRELIMINARY;	PRT;	138 AA.				
AC	Q80582;						
AC	Q80582;						
DT	01-JUN-2003 (TREMBLrel. 24, Created)						
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)						
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)						
DE	PLA(N)O.						
OS	Trimeresurus flavoviridis (habu).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;						
OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;						
OC	Viperidae; Crotalinae; Trimeresurus.						
OX	NCBI_TaxID=88087;						
RN	[1]						
SEQUENCE FROM N.A.							
RA	ChiJiwa T., Hamai S., Tsubouchi S., Oeawa T., Deshinaru M., Oda-Jeda N., Hattori S., Kinbara H., Tunazawa S., Onno M.; "Interiorland mutation of a novel phospholipase A2 from Trimeresurus flavoviridis venom and evolution of crotalinae group II phospholipase A2."						
RT	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.						
DR	EMBL; AB102729; BA6893.1; "						
DR	GO; GO:0005509; F: calcium ion binding; IEA.						
DR	GO; GO:000223; F: phospholipase A2 activity; IEA.						
DR	GO; GO:0016042; P: lipid catabolism; IEA.						
DR	InterPro; IPR001221; PhospholipaseA2.						
DR	Pfam; PF00068; Phoslip_1.						
DR	ProDom; PD000303; PhospholipaseA2; 1.						
DR	SMART; SM00085; PA2c; 1.						
DR	PROSITE; PS00119; PA2 ASP; 1.						
DR	PROSITE; PS00118; PA2 HIS; 1.						
SQ	SEQUENCE 138 AA; 15803 MW; A2F103123897ECCS CRC64;						
Query Match	44.8%; Score 321.5; DB 13; Length 138;						
Best Local Similarity	49.2%; Pred. No. 3e-30;						
Matches	61; Conservative 12; Mismatches 48; Indels 3; Gaps 2;						
QY	1 NLVQFGVMIEKMTGKSALQ-YNDYCYCIGGSHWPVDQTDWCCAHADCCYGRLEKLGC 59						
Db	17 NLQEFNRMKIMTRKGFFFTSGCYCWWGGKPKDADTRCCFVHDCCYGRV-TGCD 74						
QY	60 PKEKYLPSVSERGFCAGRITCQLLTCEDKRAALCFRNLGYTARKTAHYPAKLCGP 119						
Db	75 PKSDIYSWKTGVLTGEGTECEKQICCDRAAVCPQNRLTYKQKYMFPDFELCTDP 134						
Qy	120 TPPC 123						
Db	135 SEPC 138						
RESULT 6							
Q7ZTA8	PRELIMINARY;	PRT;	138 AA.				
AC	Q7ZTA8;						
DT	01-JUN-2003 (TREMBLrel. 24, Created)						
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)						
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)						
DE	Acidic phospholipase A2.						
OS	Crotalus viridis (Prairie rattlesnake).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;						
OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;						
OC	Viperidae; Crotalinae; Crotalus.						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RA	Tsai I.-H., Wang Y.-M., Chen Y.-H., Tu A.T.; "Geographic variations, cloning, and functional analyses of the venom						
RA	Medline=22510024; PubMed=12623078;						
RA	Tsai I.-H., Wang Y.-M., Chen Y.-H., Tu A.T.; "Geographic variations, cloning, and functional analyses of the venom						

acidic phospholipases A2 of *Crotalus viridis viridis*.";

RL Arch. Biochem. Biophys. 411:289-296 (2003).

DR EMBL:AY120877; AAH80565.1;

DR GO; GO:0005509; Fc-calchium binding; IEA.

DR GO; GO:0004623; Phospholipase A2 activity; IEA.

DR GO; GO:0016042; Lipid catalysis; IEA.

DR InterPro:IPR01211; PhospholipaseA2.

DR Pfam:PF00668; pholip; 1.

DR PRINTS:BR00389; PHOLIPASE2.

DR ProDom:PD000303; PHOSPHOLIPASEA2; 1.

DR SMART:SM00085; PACC; 1.

DR PROSITE:PS00118; PA2_HIS; 1.

DR PROSITE:PS00119; PA2_ASPP; 1.

DR PROSITE:PS00118; PA2_MN; 1.

SEQUENCE 138 AA; 44B35F1E6B29D1 CRC64;

Query Match Score 314.5; DB 13; Length 138;

Best Local Similarity 46.0%; Pred. No. 3.5e-29; Indels 3; Gaps 2;

Matches 57; Conservative 16; Mismatches 48; Indels 3; Gaps 2;

Qy 1 NLVQGYMIEKMTG-KSALQYNDYCXYCGGSHWPVDQDWCCHAHDCCYGRLEKGC 59

Db 17 NLVQFELLINKVAEKSGLLSSYAVGCGWGGYGRPQDAEDRCFVHDCCYGRV--TDCN 74

Qy 60 PKEKYLFSVSRGIFCAAGTTTCQRLTCEDKRAALCPFRNLGTYRNKRYAHYNPKLCTGP 119

Db 75 PKEKYLFSVSRGIFCAAGTTTCQRLTCEDKRAALCPFRNLGTYRNKRYAHYNPKLCTGP 134

Qy 120 TPPC 123

Db 135 PEPC 138

RESULT 8

Q7T1D1 PRELIMINARY; PRT; 138 AA.

AC Q7T1D1

DT • 01-OCT-2003 (TREMBrel. 25, Created)

DT 01-OCT-2003 (TREMBrel. 25, Last sequence update)

DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)

DE Ammodytin II.

GN AMTII.

OS Vipera berus (Common viper).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Lepidosaurs; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Viperinae; Vipera.

OX NCBITaxID:311156;

RN [1]

RP SEQUENCE FROM N.A. ID Q7T1D1; PRELIMINARY; PRT; 138 AA.

RX MEDLINE=22707820; PubMed=12823540;

RA Guillemin T., Boucher C., Garrigues T., Wisner A., Choumet V.; "Sequences and structural organization of phospholipase A2 genes from Vipera aspis aspis, V. aspis zinnikeri and Vipera berus berus venom. Identification of the origin of a new viper population based on ammodytin II heterogeneity." Eur. J. Biochem. 270:2697-2706 (2003).

Qy 1 NLVQGYMIEKMTG-KSALQYNDYCXYCGGSHWPVDQDWCCHAHDCCYGRLEKGC 59

Db 17 NLVQFELLINKVAEKSGLLSSYAVGCGWGGYGRPQDAEDRCFVHDCCYGRV--GCD 74

Qy 60 PKEKYLFSVSRGIFCAAGTTTCQRLTCEDKRAALCPFRNLGTYRNKRYAHYNPKLCTGP 119

Db 75 PKEKYLFSVSRGIFCAAGTTTCQRLTCEDKRAALCPFRNLGTYRNKRYAHYNPKLCTGP 134

Qy 120 TPPC 123

Db 135 SEQC 138

RESULT 9

Q7T1D4 PRELIMINARY; PRT; 138 AA.

AC Q7T1D4

DT 01-OCT-2003 (TREMBrel. 25, Created)

DT 01-OCT-2003 (TREMBrel. 25, Last sequence update)

DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)

DE Ammodytin II.

GN AMTII.

OS Vipera aspis (Aspic viper).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Lepidosaurs; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Viperinae; Vipera.

OX NCBITaxID:194601;

RN [1]

RP SEQUENCE FROM N.A. ID Q7T1D4; PRELIMINARY; PRT; 138 AA.

RX MEDLINE=22707820; PubMed=12823540;

RA Guillemin T., Boucher C., Garrigues T., Wisner A., Choumet V.; "Sequences and structural organization of phospholipase A2 genes from Vipera aspis aspis, V. aspis zinnikeri and Vipera berus berus venom. Identification of the origin of a new viper population based on ammodytin II heterogeneity." Eur. J. Biochem. 270:2697-2706 (2003).

Qy 1 NLVQGYMIEKMTG-KSALQYNDYCXYCGGSHWPVDQDWCCHAHDCCYGRLEKGC 59

Db 17 NLVQFELLINKVAEKSGLLSSYAVGCGWGGYGRPQDAEDRCFVHDCCYGRV--GCD 74

Qy 60 PKEKYLFSVSRGIFCAAGTTTCQRLTCEDKRAALCPFRNLGTYRNKRYAHYNPKLCTGP 119

Db 75 PKEKYLFSVSRGIFCAAGTTTCQRLTCEDKRAALCPFRNLGTYRNKRYAHYNPKLCTGP 134

Qy 120 TPPC 123

Db 135 SEQC 138

Query Match Score 312.5; DB 13; Length 138;

Best Local Similarity 47.6%; Pred. No. 6.1e-29; Mismatches 50; Indels 3; Gads 2;

Matches 59; Conservative 12; Mismatches 50; Indels 3; Gads 2;

Qy 1 NLVQGYMIEKMTG-KSALQYNDYCXYCGGSHWPVDQDWCCHAHDCCYGRLEKGC 59

Db 17 NLVQFELLINKVAEKSGLLSSYAVGCGWGGYGRPQDAEDRCFVHDCCYGRV--GCD 74

Qy 60 PKEKYLFSVSRGIFCAAGTTTCQRLTCEDKRAALCPFRNLGTYRNKRYAHYNPKLCTGP 119

Db 75 PKEKYLFSVSRGIFCAAGTTTCQRLTCEDKRAALCPFRNLGTYRNKRYAHYNPKLCTGP 134

Qy 120 TPPC 123

Db 135 SEQC 138

Page 5

PRINTS; PR00389; PHOSPHOLIPASEA2; 1.
DR Problem; DD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PAAC; 1.
DR PROSITE; PS00119; FA2_HIS; 1.
DR PROSITE; PS00118; FA2_HIS; 1.
SQ SEQUENCE 138 AA; 15556 MW; 09134B8AB3BE3723 CRC64;

Query Match 42.9%; Score 309.5; DB 13; Length 136;
Best Local Similarity 46.0%; Pred. No. 1.4e-28;
Matches 57; Conservative 14; Mismatches 50; Indels 3; Gaps 2;

QY 1 NLVQFGVMIEKMTGRKSAL-QYNDGCGYCIGGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE 59
DB 17 SLVQFEMMIKVAKRSGLFWYGAFCAGRTTCORLTCEDKRAALCFRRNLGTYNRKYAHYPNKLCTGP 74
QY 60 PKLEYLFYSYERGIFCAGRTTCAGRTTCORLTCEDKRAALCFRRNLGTYNRKYAHYPNKLCTGP 119
DB 75 PTKVSYTYSYTRNGELICEDDPCKXQVCECDRVAACFRDNIFSYNNNYKRFPAENCRGD 134

QY 120 TPPC 123
DB 135 PEPC 138

RESULT 14

Q7ZTA7 PRELIMINARY; PRT; 138 AA.
ID Q7ZTA7; STRAIN=E6a;
AC DT 01-JUN-2003 (TREMBurel. 24, Created)
DT 01-JUN-2003 (TREMBurel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBurel. 25, Last annotation update)
DE Crotalus viridis (Prairie rattlesnake).
OS Crotalyota; Metacoia; Chordata; Craniate; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scincoglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Crotalus; N.A.
RN [1] RP SEQUENCE FROM N.A.
RN [2] RP SEQUENCE FROM N.A.
RN [3] RP SEQUENCE FROM N.A.
RN [4] RP SEQUENCE FROM N.A.

RQ Tsai T.-H., Wang Y.-M.; Chen Y.H., Tu A.T.;
RA "Geographic variations, cloning, and functional analyses of the venom
acid phospholipases A(2) of *Crotalus viridis* viridis.";
RL Arch. Biochem. Biophys. 411:289-296 (2003).

PRINTS; PR000389; PHOSPHOLIPASEA2;
DR PROSITE; PS000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2; 1.
DR PROSITE; PS00119; PA2_HIS; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
SQ SEQUENCE 138 AA; 15559 MW; 04FF6D7266DB0BFE CRC64;

Query Match 42.9%; Score 309.5; DB 13; Length 138;
Best Local Similarity 45.2%; Pred. No. 1.4e-28;
Matches 56; Conservative 17; Mismatches 48; Indels 3; Gaps 2;

QY 1 NLVQFGVMIEKMTGRKSAL-QYNDGCGYCIGGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE 59
DB 17 SLVQFEMMIKVAKRSGLFWYGAFCAGRTTCAGRTTCORLTCEDKRAALCFRRNLGTYNRKYAHYPNKLCTGP 74
QY 60 PKLEYLFYSYERGIFCAGRTTCORLTCEDKRAALCFRRNLGTYNRKYAHYPNKLCTGP 119
DB 75 PTKVSYTYSYTRNGELICEDDPCKXQVCECDRVAICFRDNIPSYNSNKWLF_PKNCGD 134

QY 120 TPPC 123
DB 135 PEPC 138

Search completed: July 3, 2004, 05:17:44
Job time : 25.9925 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model!

Run on: July 3, 2004, 05:15:00 ; Search time 14.4679 Seconds
(without alignments)

Title: US-10-088-092a-30
Perfect score: 817
Sequence: 1 MKSPHVLVFLVALVTGN..... YNRKQAHYPNKLCTGPTPPC 142

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgna_6/pododata/2/iaa/5A_COMB.pep:
2: /cgna_6/pododata/2/iaa/5B_COMB.pep:
3: /cgna_6/pododata/2/iaa/6A_COMB.pep:
4: /cgna_6/pododata/2/iaa/6B_COMB.pep:
5: /cgna_6/pododata/2/iaa/pTUS_COMB.pep:
6: /cgna_6/pododata/2/iaa/backfiles1.pep:
* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	368.5	45.1	144	1	US-08-186-895-10 Sequence 10, Appl
2	368.5	45.1	144	2	US-08-888-497-37 Sequence 37, Appl
3	368.5	45.1	144	4	US-09-362-230-37 Sequence 37, Appl
4	368.5	45.1	144	5	PCT-US94-07926-37 Sequence 4, Appl
5	360.5	44.1	124	1	US-08-170-360-4 Sequence 39, Appl
6	360.5	44.1	124	1	US-08-888-497-39 Sequence 39, Appl
7	360.5	44.1	124	4	US-09-362-230-39 Sequence 2, Appl
8	360.5	44.1	124	4	US-09-569-2 Sequence 39, Appl
9	360.5	44.1	124	5	PCT-US94-07926-39 Sequence 35, Appl
10	360.5	44.1	146	2	US-08-888-497-35 Sequence 35, Appl
11	360.5	44.1	146	4	US-09-362-230-35 Sequence 35, Appl
12	360.5	44.1	146	5	PCT-US94-07926-35 Sequence 3, Appl
13	350	42.8	146	3	US-08-966-317-3 Sequence 3, Appl
14	349.5	42.8	146	3	US-09-489-770-3 Sequence 4, Appl
15	349.5	42.8	146	3	US-08-966-317-4 Sequence 4, Appl
16	349.5	42.8	146	4	US-09-489-770-4 Sequence 42, Appl
17	348	42.6	125	2	US-08-888-497-42 Sequence 42, Appl
18	348	42.6	125	4	US-09-362-230-42 Sequence 42, Appl
19	348	42.6	125	5	PCT-US94-07926-42 Sequence 5, Appl
20	321	39.3	125	1	US-08-170-360-5 Sequence 32, Appl
21	317.5	38.9	138	2	US-08-888-497-32 Sequence 32, Appl
22	317.5	38.9	138	4	US-09-362-230-32 Sequence 32, Appl
23	317.5	38.9	138	5	PCT-US94-07926-32 Sequence 30, Appl
24	314.5	38.5	137	2	US-08-888-497-30 Sequence 30, Appl
25	314.5	38.5	137	4	US-09-362-230-30 Sequence 30, Appl
26	314.5	38.5	137	5	PCT-US94-07926-30 Sequence 40, Appl
27	299.5	36.7	118	2	US-08-888-497-40 Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-08-186-895-10
; Sequence 10, Application US/08186895
; Patent No. 5538885
; GENERAL INFORMATION:
; APPLICANT: Hollis, Melvyn
; APPLICANT: Needham, Maurice R.C.
; APPLICANT: Gooding, Clare
; APPLICANT: Grosveld, Franklin G.
; TITLE OF INVENTION: Expression Systems
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cushman, Darby & Cushman
; STREET: 1115 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Parent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,895
; FILING DATE: 27-JAN-1994
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/046,383
; FILING DATE: 09-APR-1993
; APPLICATION NUMBER: US/07/810,414
; ATTORNEY/AGENT INFORMATION:
; NAME: Kokulis, Paul N.
; REGISTRATION NUMBER: 1,6,773
; TELECOMMUNICATION INFORMATION:
; TELEFAX: 202-861-3000
; TELEFAX: 202-822-0944
; TELEFAX: 6714227 CUSH
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 144 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-186-895-10
Query Match 45.1%; Score 368.5; DB 1;
Best Local Similarity 52.1%; Pred No. 5.1e-32;
Matches 73; Conservative 12; Mismatches 46; Indels 9; Gaps 2;

Query 12 LLVALVT-----GNIYQFGVNLIEKMTGK-SALQYNDGGCCTGCGTGSHTWVDDCDWCC 62
 Database 5 LLLAVMIFGILQAHGNLYNFRHMKLITGEAALSYGFGCHGCVgGRGSPKDADTRCC 64
 Query 63 HAHDCCYGRLEKLGCEPKLEYKLFSVSERGIFCAGRITCQLTCECDKRAALCFPRNLGT 122
 Database 65 VTHDCCYKRLEKRGGTGKFLPSYKFSNSGSRITCAKQDSRSQLCEDKAATCFARNKTT 124

Query 123 YNRKYAHYPNLCLTGTPPC 142
 Database 125 YNRKYQYSNKHCRGSTPRC 144

Result 3 US-09-362-230-37
 Sequence 37, Application US/09362230
 Patent No. 6352849

General Information:
 Applicant: Tischfield, Jay A.
 Address: Ruden, Barnett, McClosky, Smith, Schuster & Seilhamer, Jeffrey J.
 Title of Invention: Mammalian Phospholipase A2 Nucleotide Sequences and Low Molecular Weight Amino Acid Sequences

Title of Invention: Encoded Therby, Antisense Sequences and Nucleotide Sequences Having Internal Ribosome Binding Sites

Number of Sequences: 44
 Correspondence Address:
 Applicant: Tischfield, Jay A.
 Address: Ruden, Barnett, McClosky, Smith, Schuster & Seilhamer, Jeffrey J.
 Title of Invention: Mammalian Phospholipase A2 Nucleotide Sequences and Low Molecular Weight Amino Acid Sequences
 Title of Invention: Encoded Therby, Antisense Sequences and Nucleotide Sequences Having Internal Ribosome Binding Sites

Number of Sequences: 44
 Correspondence Address:
 Addressee: Ruden, Barnett, McClosky, Smith, Schuster & Seilhamer, Jeffrey J.
 Title of Invention: Mammalian Phospholipase A2 Nucleotide Sequences and Low Molecular Weight Amino Acid Sequences
 Title of Invention: Encoded Therby, Antisense Sequences and Nucleotide Sequences Having Internal Ribosome Binding Sites

Address: Russell, PA
 Street: 200 East Broward Boulevard
 City: Fort Lauderdale
 State: FL
 Country: USA
 Zip: 33301

Computer Readable Form:
 Medium Type: Floppy disk
 Computer: IBM PC Compatible
 Operating System: PC-DOS/MS-DOS
 Software: Patentn Release #1.0., Version #1.25
 Application Number: US/08/888,497
 Filing Date:
 Classification:
 Prior Application Data:
 Application Number: US/08/651,405
 Filing Date:
 Application Number: US 08/097,354
 Filing Date: 26-JUL-1993
 Attorney/Agent Information:
 Name: Manso, Peter J.
 Registration Number: 32,264
 Reference/DoCKET Number: IN21044-5
 Telecommunication Information:
 Telephone: 305-527-2498
 Telefax: 305-764-4996
 Information for SEQ ID NO: 37:
 Sequence Characteristics:
 Length: 144 amino acids
 Type: amino acid
 Strandedness: single
 Topology: linear
 Molecule type: protein

US-08-888-497-37

Query Match 45.1%; Score 368.5; DB 4; Length 144;
 Best Local Similarity 52.1%; Pred. No. 5.1e-32;
 Matches 73; Conservative 12; Mismatches 46; Indels 9; Gaps 2;

Query 12 LLVALVT-----GNIYQFGVNLIEKMTGK-SALQYNDGGCCTGCGTGSHTWVDDCDWCC 62
 Database 5 LLLAVMIFGILQAHGNLYNFRHMKLITGEAALSYGFGCHGCVgGRGSPKDADTRCC 64
 Query 63 HAHDCCYGRLEKLGCEPKLEYKLFSVSERGIFCAGRITCQLTCECDKRAALCFPRNLGT 122
 Database 65 VTHDCCYKRLEKRGGTGKFLPSYKFSNSGSRITCAKQDSRSQLCEDKAATCFARNKTT 124

Query 12 LLVALVT-----GNIYQFGVNLIEKMTGK-SALQYNDGGCCTGCGTGSHTWVDDCDWCC 62
 Database 5 LLLAVMIFGILQAHGNLYNFRHMKLITGEAALSYGFGCHGCVgGRGSPKDADTRCC 64
 Query 63 HAHDCCYGRLEKLGCEPKLEYKLFSVSERGIFCAGRITCQLTCECDKRAALCFPRNLGT 122

Query Match 45.1%; Score 368.5; DB 2; Length 144;
 Best Local Similarity 52.1%; Pred. No. 5.1e-32;
 Matches 73; Conservative 12; Mismatches 46; Indels 9; Gaps 2;

Query 123 YNRKYAHYPNLCLTGTPPC 142
 Database 125 YNRKYQYSNKHCRGSTPRC 144

RESULT 4

PCP-US94-07926-37

Sequence 37, Application PC/TUS9407926

GENERAL INFORMATION

APPLICANT: Tischfield, Jay A.

APPLICANT: Seilhamer, Jeffrey J.

TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide Sequences and Low Molecular Weight Amino Acid Sequences Encoded Thereby, Antisense Sequences and Nucleotide Sequences Having Internal Ribosome Binding Sites

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & Associates

STREET: 200 East Broward Boulevard

CITY: Fort Lauderdale

STATE: FL

COUNTRY: USA

ZIP: 33301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/07926

FILING DATE: 15-JUL-1994

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/097,354

FILING DATE: 26-JUL-1993

ATTORNEY/AGENT INFORMATION:

NAME: Manso, Peter J.

REGISTRATION NUMBER: 32,264

REFERENCE/DOCKET NUMBER: IN21044-5

TELECOMMUNICATION INFORMATION:

TELEFAX: 305-527-2498

TELEPHONE: 305-764-4996

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 144 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

PCP-US94-07926-37

Query Match 45.1%; Score 368.5; DB 5; Length 144;

Best Local Similarity 52.1%; Prec. No. 5.1e-32;

Matches 73; Conservative 12; Mismatches 46; Indels 9; Gaps 2;

Qy 12 LLVALVT-----GNIQFGYMIERTGK-SALQNDYGYCGTCGSHWVVDQTDWC 62

Db 5 LLLAVIMFGLQAHGNLYNFRMILKTGKEAALSYGFGYHCGVGRGSQPKDADRC 64

Qy 63 HAHDCCYGRLEKLGCEPKLEYKLFSVSRGTFCAAGRITCQRLLTCECDKRAAICFRENLT 122

Db 65 VTHDCCYGRLEKLGCEPKLEYKLFSVSRGTFCAAGRITCQRLLTCECDKRAAATCFARNKT 124

RESULT 6

US-08-888-497-39

Sequence 39, Application US/08888497

GENERAL INFORMATION:

APPLICANT: Tischfield, Jay A.

APPLICANT: Seilhamer, Jeffrey J.

TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide Sequences and Low Molecular Weight Amino Acid Sequences

TITLE OF INVENTION: Sequences and Nucleotide Encoded Thereby, Antisense Sequences and Nucleotide Sequences Having Internal Ribosome Binding Sites

TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

RESULT 7
 US-09-362-230-39
 Sequence 39 Application US/09362239
 Patent No. 6352849
 GENERAL INFORMATION:
 APPLICANT: Tischfield, Jay A.
 TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide Sequences and Low Molecular Weight Amino Acid Sequences Having Internal Ribosome Binding Sites
 TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide Sequences Having Internal Ribosome Binding Sites
 NUMBER OF SEQUENCE: 44
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ruder, Barnett, McClosky, Smith, Schuster & Russell, PA
 STREET: 200 East Broward Boulevard
 CITY: Fort Lauderdale
 STATE: FL
 COUNTRY: USA
 ZIP: 33301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/362/230
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/651,405
 FILING DATE: 26-JUL-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Manso, Peter J.
 REGISTRATION NUMBER: 32,264
 REFERENCE/DOCKET NUMBER: IN21044-5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 305-764-4996
 TELEFAX: 305-764-4996
 INFORMATION FOR SEQ ID NO: 39:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 124
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-888-497-39

Query Match 44.1%; Score 360.5; DB 2; Length 124;
 Best Local Similarity 55.6%; Pred. No. 3.1e-31;
 Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;

Qy 20 NLVQFGVMTERMTGK-SALQVNDYGGCYCGIGSHWPVQDTDWCHAHDCGYPLEKLGCE 78
 Db 1 NLVNPHRMKLTGKEAALSYGFGCHGVGRGSPKDATDRCVTHCCYKELEKRCCG 60

Qy 79 PKLEYLFSYSERGIFCAGRTTCORLTCEBDKRALCFRRNLTYNRYAHYNPKLCGP 138
 Db 61 TKFLSYKFNSGSRITCAKODSCRSQLCBDKAATCPARNKTTYNKKYQYTSNKHCRGS 120

Qy 139 TPPC 142
 Db 121 TPRC 124

RESULT 8
 US-09-740-569-2
 Sequence 2 Application US/09740569
 Patent No. 6475484
 GENERAL INFORMATION:
 APPLICANT: Weiss, Jerrold
 APPLICANT: Liang, Ning-Sheng
 TITLE OF INVENTION: ANTI-BACTERIAL GROUP IIA PHOSPHOLIPASE A2 AND METHODS OF USE THEREFOR
 FILE REFERENCE: 5986/1E91TUS1
 CURRENT APPLICATION NUMBER: US/09/740,569
 CURRENT FILING DATE: 2000-12-18
 PRIOR APPLICATION NUMBER: US 60/172,467
 PRIOR FILING DATE: 199-12-17
 NUMBER OF SEQ ID NO: 5
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 2
 LENGTH: 124
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-740-569-2

Query Match 44.1%; Score 360.5; DB 4; Length 124;
 Best Local Similarity 54.8%; Pred. No. 3.1e-31;
 Matches 68; Conservative 11; Mismatches 44; Indels 1; Gaps 1;

Qy 20 NLVQFGMMIERTMKGK-SALQNDYCGCCGSHWPVDOTDWCCCHAHDCCYGRLEKIGCE 78
 Db 1 NLVNFHRLLKLITGKEAALSQYGFVCHCAGRSKPDOTDRCCVTHIDCYRKLEKRG 60

Qy 79 PKLEYLPSVSERGFCAGRTTCORLTCDFKRALCFPRRNLCGTYNRYAHYPNKLCTGP 138
 Db 61 TKPLSYKFNSKSRITCAKDSCRSQLCBDDKAATCFARNKCTYNNKQYXSNKHCRGS 120

Qy 139 TPPC 142
 Db 121 TPRC 124

RESULT 9
 Sequence 39, Application PC/US9407926-39
 GENERAL INFORMATION:
 APPLICANT: Tischfield, Jay A.
 TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide Sequences and Low Molecular Weight Amino Acid Sequences
 TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide Sequences Having Internal Ribosome Binding Sites
 NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Rudden, Barnett, McClosky, Smith, Schuster &
 STREET: 200 East Broward Boulevard
 CITY: Fort Lauderdale
 STATE: FL
 COUNTY: USA
 ZIP: 33301

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/888,497
 FILING DATE: 15-JUL-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Manso, Peter J.
 REGISTRATION NUMBER: 32,264
 REFERENCE/DOCKET NUMBER: IN21044-5

PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/07926
 FILING DATE: 26-JUL-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Manso, Peter J.
 REGISTRATION NUMBER: 32,264
 REFERENCE/DOCKET NUMBER: IN21044-5

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 305-527-2698
 TELEFAX: 305-764-4996

INFORMATION FOR SEQ ID NO: 39:
 LENGTH: 124 amino acids
 SEQUENCE CHARACTERISTICS:
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein

Query Match 44.1%; Score 360.5; DB 2; Length 146;
 Best Local Similarity 47.9%; Pred. No. 3.1e-31; Mismatches 18; Indels 7; Gaps 3;

Qy 6 VLVFLCLVAL----VGNLVPFEMTRMTGSA-LOYNDYGCYGTGGSIWPVDQD 59
 Db 1 :::::
 3 VLLLAIVIMAFGSIQVQSSLLEGQMLFKTGADYSYGFIGGCCYVGGRSPKDADT 62

Qy 60 WCCHAHDCYCGRLEKLGCEPKLEYLPSVSERGFCAGRTTCORLTCDFKRALCFRR 118
 Db 63 WCCVTHDCYCNRLEKGCYGTGPKTFYKSYRGGQISCTNQDSCKQLCQCDKAACCPAR 122

Qy 119 NLGTYNRYAHYPNKLCTGTPPC 142
 Db 123 NRKSYSLKQYPNFKGRGPSC 146

RESULT 11

Qy 20 NLVQFGMMIERTMKGK-SALQNDYCGCCGSHWPVDOTDWCCCHAHDCCYGRLEKIGCE 78
 Db 1 NLVNFHRLLKLITGKEAALSQYGFVCHCAGRSKPDOTDRCCVTHIDCYRKLEKRG 60

Qy 79 PKLEYLPSVSERGFCAGRTTCORLTCDFKRALCFPRRNLCGTYNRYAHYPNKLCTGP 138
 Db 61 TKPLSYKFNSKSRITCAKDSCRSQLCBDDKAATCFARNKCTYNNKQYXSNKHCRGS 120

US-09-362-230-35 Sequence 35, Application US/09362230
 GENERAL INFORMATION: Patent No. 6352849
 APPLICANT: Tischfield, Jay A.
 TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide Sequences and Low Molecular Weight Amino Acid Sequences Having Internal Ribosome Binding Sites
 NUMBER OF SEQUENCES: 44
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & Russell PA
 STREET: 200 East Broward Boulevard
 CITY: Fort Lauderdale
 STATE: FL
 COUNTRY: USA
 ZIP: 33301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/362,230
 FILING DATE:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/888,497
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION NUMBER: US/09/362,230
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Manso, Peter J.
 REGISTRATION NUMBER: 32,264
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 305-764-4996
 TELEFAX: 305-527-2498
 TELEFAX: 305-764-4996
 INFORMATION FOR SEQ ID NO: 35:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 146 amino acids
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US94-07926-35
 Query Match 44.1%; Score 360.5; DB 4; Length 146;
 Best Local Similarity 47.9%; Pred. No. 3.7e-31; Indels 7; Gaps 3;
 Matches 69; Conservative 18; Mismatches 50; Indels 7; Gaps 3;
 Qy 6 VVFLCLVL---VTRGLVQFGMIRKMTGSA-LQYNDGCGGSHMPVDQD 59
 Db 3 VLLLAIVMAFGSLOQVGSLLFQMLFLKTGRADYSVGFGCHCAGGSGPKDAD 62
 Qy 60 WCCHAHDCCYGRLEKLGCBPLKELYLFSVSRGLPCA-GRTTCORLTCDCRAALCPR 118
 Db 63 WCCVTHDCCNRLERGCKFVTKFSTGGQISCSNQDSRKQLQCDKAAECPAR 122
 RESULT 13 US-08-966-317-3
 Sequence 3, Application US/08966317
 Patent No. 6103469
 GENERAL INFORMATION:
 ADDRESSEE: Hawkins, Phillip R.
 APPLICANT: Bandman, Olga
 APPLICANT: Guglieri, Purvi
 APPLICANT: Shah, Purvi
 APPLICANT: Corley, Neil C.
 TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Dr.
 CITY: Palo Alto

RESULT 12 PCT-US94-07926-35
 Sequence 35, Application PC/TUSS9407926
 GENERAL INFORMATION:
 APPLICANT: Tischfield, Jay A.
 APPLICANT: Sellhamer, Jeffrey J.
 TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide Sequences and Low Molecular Weight Amino Acid Sequences Having Internal Ribosome Binding Sites

STATE: CA
CITY: USA
ZIP: 94304
COMPUTER READABLE FORM:
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/966,317
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0403 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 984837
US-09-966-317-3

Query Match 42.8%; Score 350; DB 3; Length 146;
Best Local Similarity 53.1%; Pred. No. 4.9e-30;
Matches 68; Conservative 9; Mismatches 49; Indels 2; Gaps 2;

Query 17 VTNGLVQPGVMIKMTGKSA-LOYNQYCGIGGSHPVDTDWCCHAHDCCYGRLEKLJ 75
Db 19 VQGNIAQFQEMIRLKTRGAEELSYAFGCCGGKGSPKDADTRCCVTHDCYCSLEKS 78

Query 17 VTNGLVQPGVMIKMTGKSA-LOYNQYCGIGGSHPVDTDWCCHAHDCCYGRLEKLJ 75
Db 19 VQGNIAQFQEMIRLKTRGAEELSYAFGCCGGKGSPKDADTRCCVTHDCYCSLEKS 78

Query 76 GCEPKLKLXFLSVSERGIFC-AGRRTTCQRLTCECDRAALCPRNLTGTYNRYKAHYPNKL 134
Db 79 GCGTKLLXFLKYSHQGQ1TCSANQNSCQRKLQCDKAAEFCARNKTYSLKTYQFPNMF 138

RESULT 15
US-09-966-317-4

Query 135 CTGPPPPC 142
Db 139 CKGKKPKC 146

RESULT 14
US-09-989-770-3

GENERAL INFORMATION
PATENT NO. 6,399,910
APPLICANT: Hawkins, Phillip R.
APPLICANT: Bandman, Olga
APPLICANT: Guegler, Karl J.
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.

NUMBER OF SEQUENCES: 4
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
COUNTRY: CA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/966,317
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36749
REFERENCE/DOCKET NUMBER: PF-0403 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 204319
US-08-966-317 4

Query Match 42.8%; Score 349.5; DB 3; Length 146;
Best Local Similarity 47.2%; Pred. No. 5.6e-30;
Matches 68; Conservative 18; Mismatches 51; Indels 7; Gaps 3;

Qy	6	VLVFICLVAL-----VIGNLVQFGVMERMTGKSA-LQYNDYGCYCGIGSHWPVDQD	59
Db	3	VILLAVIMAFGSTQVGSSLEPGKMLFKTGKADSYGFVGCHGVGERGSPKDATD	62
Qy	60	WCCHAHDCCYGRLEKLGEFPLKYLFSYSERGIFCA-GRTTCQLRLTCEDKRAALCFRR	118
Db	63	WCCVTHDCCNVRLEKRGCTKFLTYKSFYRGQQLSCSTNQDSRKQLCQCDKAACFCAR	122
Qy	119	NLGTYNRKYAHYPNKLCTGTPPC	142
Db	123	NKKSYSLKCYOFYLNKFCKGKTPSC	146

Search completed: July 3, 2004, 05:18:46
Job time : 15.4679 secs

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OM protein - protein search, using sw model

Run on: July 3, 2004, 05:17:51 ; Search time 50.3698 seconds

(without alignments)

Title: US-10-088-092A-30

Perfect score: 817

Sequence: 1 MKSPHVLVFLCLVALVTGN YNRKYAHYPNKLCTGPTPPC 142

Scoring table: BL0SUM62

Searched: Gapext 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 1276540

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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3: /cgn2_6_ptodata/2/pubcaa/US06_NEW_PUB.pep;*

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11: /cgn2_6_ptodata/2/pubcaa/US09C_NEW_PUBCOMB.pep;*

12: /cgn2_6_ptodata/2/pubcaa/US10A_NEW_PUB.pep;*

13: /cgn2_6_ptodata/2/pubcaa/US10A_PUBCOMB.pep;*

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16: /cgn2_6_ptodata/2/pubcaa/US10C_NEW_PUB.pep;*

17: /cgn2_6_ptodata/2/pubcaa/US60_NEW_PUB.pep;*

18: /cgn2_6_ptodata/2/pubcaa/US60_PUBCOMB.pep;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	817	100.0	154	10-US-09-971-456B-8	Sequence 8, Appli
2	370	45.3	164	9-US-09-925-300-1010	Sequence 10, Appli
3	368.5	45.1	144	10-US-09-975-456B-6	Sequence 6, Appli
4	368.5	45.1	144	14-US-10-205-823-325	Sequence 325, Appli
5	368.5	45.1	144	15-US-10-116-275-269	Sequence 269, Appli
6	360.5	44.1	124	14-US-10-255-576-2	Sequence 2, Appli
7	350	42.8	146	9-US-09-993-999-8	Sequence 8, Appli
8	350	42.8	146	13-US-10-124-591-3	Sequence 3, Appli
9	349.5	42.8	138	12-US-09-917-805-7	Sequence 7, Appli
10	349.5	42.8	146	13-US-10-124-591-4	Sequence 4, Appli
11	345.5	42.3	138	12-US-09-917-805-6	Sequence 6, Appli
12	325.5	39.8	138	12-US-09-917-805-2	Sequence 2, Appli
13	317.5	38.9	138	10-US-09-945-456B-9	Sequence 9, Appli
14	310.5	38.0	145	9-US-09-969-384-17	Sequence 17, Appli
15	310.5	38.0	145	10-US-09-975-456B-7	Sequence 7, Appli

ALIGNMENTS

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RESULT 1
US-09-975-456B-8
; Sequence 8, Application US/09975456B
; GENERAL INFORMATION:
; APPLICANT: LAZDUNSKI, MICHAEL
; APPLICANT: LAMBEAU, GERARD
; APPLICANT: VALENTIN, EMMANUEL
; TITLE OF INVENTION: NOVEL MAMMALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2
; FILE REFERENCE: 1478-R0
; CURRENT APPLICATION NUMBER: US/09/975, 456B
; CURRENT FILING DATE: 2002-08-27
; PRIORITY APPLICATION NUMBER: 10-239, 491
; PRIORITY FILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin version 2.1
; SEO_ID NO: 8
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-975-456B-8

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Query Match 100.0%; Score 817; DB 10; Length 154;

Best Local Similarity 100 %; Pred. No. 8 9e-82;

Matches 142; Conservative 0; Missmatches 0; Indels 0; Gaps 0;

Qy 1 MKSPHVLVFLCLVALVTGNIVQFCVMTGKSAQLYNDGCYCYGIGGSHWPVDQTDW 60
Db 13 MKSPHVLVFLCLVALVTGNIVQFCVMTGKSAQLYNDGCYCYGIGGSHWPVDQTDW 72

Qy 61 CCHAHCYCYGRLEKPLKLYFVSYSERGIFCAAGRITCQRLTCECDKRAALCFRNL 120
Db 73 CCHAHCYCYGRLEKPLKLYFVSYSERGIFCAAGRITCQRLTCECDKRAALCFRNL 132

Qy 121 GTYNTRKAYHPNKLCTGTPPC 142
Db 133 GTYNTRKAYHPNKLCTGTPPC 154

RESULT 2
 US-09-925-300-1010
 ; Sequence 1010, Application US/09925300
 ; Patent No. US20020151681A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Craig Rosen,
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PA101.
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05988
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 1890
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1010
 ; LENGTH: 164
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-925-300-1010

Query Match 45.3%; Score 370; DB 9; Length 164;
 Best Local Similarity 50.3%; Pred. No. 1.5e-32;
 Matches 75; Conservative 10; Mismatches 54; Indels 10; Gaps 2;

Qy 4 PHVVLFLCLLYALVT-----GNYLQFGVMIEKMTGK-SALQYNDGYCGIGGSHEW 53
 Db : 16 PRTLTMKTLILLAVIMIFGILQAHNLVNPHRMKLTKLTKEAALSFGYCHGVGERGS 75

Qy 54 PVDQDWDCCAHDCCYGRLEKLGCEPKLEYLFVSYSERGFCGRTTCQRLTECDRAA 113
 Db 76 PKDATDRCCYTHDCCYKRLERKGCGTKEFYSKFGNSITCAQDSCRSQCECDKA 135

Qy 114 LCFFRNLLGTNRYAHYPNKLCTGPTPPC 142
 Db 136 TCFARNKTTINKKYQQYSNKHCRGSTPRC 164

RESULT 3
 US-09-975-456B-6
 ; Sequence 6, Application US/09975456B
 ; Publication No. US2003073087A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LAZDINSKI, MICHEL
 ; APPLICANT: LAMBAU, GERARD
 ; APPLICANT: VALENTIN, EMMANUEL
 ; TITLE OF INVENTION: NOVEL MAMMALIAN SECRETED GROUP I IF PHOSPHOLIPASE A2
 ; FILE REFERENCE: 1478-R-00
 ; CURRENT FILING DATE: 2002-08-27
 ; PRIOR FILING DATE: 2000-10-11
 ; NUMBER OF SEQ ID NOS: 10
 ; SEQ ID NO 6
 ; SOFTWARE: PatentIn version 2.1
 ; LENGTH: 144
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-975-456B-6

Query Match 45.1%; Score 368.5; DB 10; Length 144;
 Best Local Similarity 52.1%; Pred. No. 1.8e-32;
 Matches 73; Conservative 12; Mismatches 46; Indels 9; Gaps 2;

Qy 12 LIVALVTT-----GNYLQFGVMIEKMTGK-SALQYNDGYCGIGGSHEWPDQTDMCC 62
 Db 5 LLAVIMIFGILQAHNLVNPHRMKLTKLTKEAALSFGYCHGVGRGSPPDATDRCC 64

Qy 63 HAHDCCYGRLEKLGCEPKLEYLFVSYSERGFCGRTTCQRLTECDRAALCPRNULT 122
 Db 65 VTHDCCYKRLEKLGCEPKLEYLFVSYSERGFCGRTTCQRLTECDRAATCFARNKTT 124

RESULT 4
 US-10-205-823-325
 ; Sequence 325, Application US/10205823
 ; Publication No. US20030108263A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schlegel, Robert
 ; APPLICANT: Monana, John E.
 ; APPLICANT: Endge, Wilson O.
 ; APPLICANT: Gannavarapu, Manjula
 ; APPLICANT: Gorbatcheva, Bella
 ; APPLICANT: Hoersch, Sebastian
 ; APPLICANT: Kamatkar, Shubhangi
 ; APPLICANT: Wongsey, Angela M.
 ; APPLICANT: Giatt, Karen
 ; APPLICANT: Zhao, Xumei
 ; APPLICANT: Anderson, Dustin
 ; APPLICANT: FILE REFERENCE: MRI-044
 ; CURRENT FILING DATE: 2002-07-15
 ; PRIOR APPLICATION NUMBER: 60/307,982
 ; PRIOR FILING DATE: 2001-07-15
 ; PRIOR APPLICATION NUMBER: 60/314,356
 ; PRIOR FILING DATE: 2001-08-22
 ; PRIOR APPLICATION NUMBER: 60/325,020
 ; PRIOR FILING DATE: 2001-09-25
 ; PRIOR APPLICATION NUMBER: 60/341,746
 ; PRIOR FILING DATE: 2001-12-12
 ; PRIOR APPLICATION NUMBER: 60/362,158
 ; NUMBER OF SEQ ID NOS: 455
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 325
 ; LENGTH: 144
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-205-823-325

Query Match 45.1%; Score 368.5; DB 14; Length 144;
 Best Local Similarity 52.1%; Pred. No. 1.8e-32;
 Matches 73; Conservative 12; Mismatches 46; Indels 9; Gaps 2;

Qy 12 LIVALVTT-----GNYLQFGVMIEKMTGK-SALQYNDGYCGIGGSHEWPDQTDMCC 62
 Db 5 LLAVIMIFGILQAHNLVNPHRMKLTKLTKEAALSFGYCHGVGRGSPPDATDRCC 64

Qy 63 HAHDCCYGRLEKLGCEPKLEYLFVSYSERGFCGRTTCQRLTECDRAALCPRNULT 122
 Db 65 VTHDCCYKRLEKLGCEPKLEYLFVSYSERGFCGRTTCQRLTECDRAATCFARNKTT 124

RESULT 5
 US-10-116-275-269
 ; Sequence 269, Application US/10116275
 ; Publication No. US2003021147A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Elan Pharmaceutical Technology
 ; APPLICANT: O'Mahony, Daniel J.
 ; APPLICANT: Brayden, David
 ; APPLICANT: Byrne, Daragh

APPLICANT: Lambkin, Imelda
 APPLICANT: Higgins, Lisa
 TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and Compositions Targeting Peyer's Patches and M Cell Receptors
 FILE REFERENCE: E106/20087
 CURRENT APPLICATION NUMBER: US/10/116,275
 CURRENT FILING DATE: 2002-10-04
 NUMBER OF SEQ ID NOS: 349
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 269
 LENGTH: 144
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-116-275-269

Query Match 45.1%; Score 368.5; DB 15; Length 144;
 Best Local Similarity 52.1%; Pred: No. 1..8e-32; Mismatches 46; Indels 9; Gaps 2;
 Matches 73; Conservative 12; SEQ ID NOS: 349
 Software: PatentIn version 3.1

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Qy 12 LLVALVT-----GNIYQGYNTEKRMGK-SALQYNDYGGCYCGIGGSSHHWPVTDQTDMC 62
Db 5 LLLAVIMFLQLQARGNLNFHRHLKLTKLGEPEPKLEKYLEVSVERGIFCGRTRTCORLTCDXRAALCFRRNLGT 64
Qy 63 HAHDCCYGRLEKLGEGPKEKLYSYKFSNSGSRITCAKDSCRSOLCEAAATCFARNKTT 122
Db 65 VTHDCCYKRLEKRGKGTKFLSYKFSNSGSRITCAKDSCRSOLCEAAATCFARNKTT 124
Qy 123 YNRKAYHINWNLCTGTPC 142
Db 125 YNKKCYQQYSNKHCRSSTPRC 144
  
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RESULT 6
 US-10-102-575-2
 Sequence 2, Application US/10255576
 Publication No. US20030161822A1
 GENERAL INFORMATION:
 APPLICANT: Weiss, Jerryd
 APPLICANT: Eisbach, Peter
 APPLICANT: Liang, Ning-Sheng
 TITLE OF INVENTION: ANTIBACTERIAL GROUP IIA PHOSPHOLIPASE A2 AND METHODS OF USE THERE

FILE REFERENCE: 5986/1E917US1
 CURRENT APPLICATION NUMBER: US/10/255,576
 CURRENT FILING DATE: 2002-09-25
 PRIOR APPLICATION NUMBER: US/09/740,569
 PRIOR FILING DATE: 2000-12-18
 PRIOR APPLICATION NUMBER: US 60/172,467
 PRIOR FILING DATE: 1999-12-17
 NUMBER OF SEQ ID NOS: 5
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 2
 LENGTH: 124
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-255-575-2

Query Match 44.1%; Score 360.5; DB 14; Length 124;
 Best Local Similarity 54.8%; Pred: No. 1..2e-31; Mismatches 44; Indels 1; Gaps 1;
 Matches 68; Conservative 11; SEQ ID NOS: 5
 Software: PatentIn version 3.1

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Qy 20 NLVQFGVMTK-SALQYNDYGGCYCGIGGSSHHWPVTDQTDMCCHADCCYGRLEXLGCB 78
Db 1 NLVNFHRLKLTKLGEPEPKLEKYLEVSVERGIFCGRTRTCORLTCDXRAALCFRRNLGT 138
Qy 79 PKLCKYLFRSERIFCAARGRTTCORLTCDXRAALCFRRNLGT 138
Db 61 TFKLSYKFSNSKSRSITCAKDSCRSOLCECDKAATCPARNKKTNYKYYIISNKHCRGS 120
Qy 139 TPPC 142
Db 121 TPRC 124
  
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RESULT 7
 US-09-993-999-8
 Sequence 8, Application US/0993999
 Patent No. US201010891A1
 GENERAL INFORMATION:
 APPLICANT: Ho, I-Cheng
 APPLICANT: Arm, Jonathan P.
 APPLICANT: Austen, K. Frank
 APPLICANT: Glimcher, Lauri H.
 TITLE OF INVENTION: Phospholipase A2 Group Preferentially Expressed in Th2 Cells
 FILE REFERENCE: H01-046
 CURRENT APPLICATION NUMBER: US/09/993,999
 CURRENT FILING DATE: 2001-11-06
 PRIOR APPLICATION NUMBER: 60/246,316
 PRIOR FILING DATE: 2000-11-06
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 8
 LENGTH: 146
 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-993-999-8

Query Match 42.8%; Score 350; DB 9; Length 146;
 Best Local Similarity 53.1%; Pred: No. 2e-30; Mismatches 9; Indels 2; Gaps 2;
 Matches 68; Conservative 49; SEQ ID NOS: 8
 Software: FastSEQ for Windows Version 4.0

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Qy 17 VTNGLVQFGVMTKSGSA-LQYNDYGGCYCGIGGSSHHWPVTDQTDMCCHADCCYGRLEXKL 75
Db 19 VQGNIAQFGENTIRLKGRKRSLSAYGCHGLGGGSPKDAEDRCVTHDCYCYSKLES 78
Qy 76 GCEPKLCKYLFSVSERGIFC-AGRITACORLTCECDKRAALCFRRNLGTNRYKAYHPNKL 134
Db 79 GCGTKLCKYKSHQGQQTCSANONSCQRKLQCDKAALCFAVNKKTSLKQYPNMF 138
Qy 135 CTGPTPPC 142
Db 139 CKGKKKRC 146
  
```

TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Dr.
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ For Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/124,591
 FILING DATE: 16-Apr-2002
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/489,770
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US/09/489,770
 FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
REGISTRATION NUMBER: 16,749
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-945-4166

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 14; amino acids
STRANDEDNESS: single
TOPOLogy: linear

IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 984837

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-124-591-3

Query Match 42.8%; Score 350; DB 13; Length 146;
Best Local Similarity 51.1%; Pred. No. 2e-30; Indels 2; Gaps 2;
Matches 68; Conservative 9; Mismatches 49;

Qy 17 VTNLIVQFGMIEKMTGKSA-LQNDYGYCIGIGGSHRPVDQTDWCCHAHDCCYGRLEKL 75
Db 19 VQGNIAQFGMIRLKTGGRBELSAYFGCIGGKGSKPDAADRCCYTHDCYCYSLEKS 78

Qy 76 GCEPKPLEKYLFSVSRGIFC-AGITTCQFLTCBDCDKRAALCFPRNLGTYNRKTAHYPNKL 134
Db 79 GCGTLLKRYKSHHQGGQTICRSANQNSCQRLLCQCDKAACFARNKCTYSLYXQFPNMF 138

Qy ^ 135 CTGPTPPC 142
Db 139 CKGRKPKC 146

RESULT 9
US-09-917-805-7

Sequence 7, Application US-099117805
Publication No. US20040173573A1
GENERAL INFORMATION:
APPLICANT: STYME, Sten
APPLICANT: STAHL, Ulf
APPLICANT: EK, Bo
APPLICANT: SJODAHL, Staffan
TITLE OF INVENTION: PLANT ENZYME AND USE THEREOF
FILE REFERENCE: STYME=1

CURRENT APPLICATION NUMBER: US-09-917,805
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 09/155,124
PRIOR FILING DATE: 1999-03-02
PRIOR APPLICATION NUMBER: PCT/SE97/00554
PRIOR FILING DATE: 1997-03-27
PRIOR APPLICATION NUMBER: 9601237.2
PRIOR FILING DATE: 1996-03-29
NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 7
LENGTH: 138
TYPE: PRT
ORGANISM: Bothrops jararacussu

US-09-917-805-7

Query Match 42.8%; Score 349.5; DB 12; Length 138;
Best Local Similarity 48.2%; Pred. No. 2.2e-30; Indels 3; Gaps 2;
Matches 66; Conservative 15; Mismatches 53;

Qy 7 LVFLCLVALVLTQFGMIEKMTGKSA-LQNDYGYCIGIGGSHRPVDQTDWCCHAH 65
Db 4 LWIMAVLVLVQGYEDLWQFGMILKETGKLFPEPYTTGCGCNGQGQPKDADTRCCFVH 63

Qy 66 DCCYGRLEKLGCEPKLEKYLFSVSRGIFCAGRTTCQRLTCECDKRALCFRNLGTYNR 125
Db 123 NRKSYSLKQFYLNKESKGKTPSC 146

RESULT 10
US-10-124-591-4

Sequence 4, Application US-10124591
Publication No. US20020177208A1
GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
Bandman, Olga
Guegler, Kari J.
Shah, Purvi
Corley, Neil C.

TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
ZIP: 94304

COMPUTER FORM:
MEDIUM: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-10-124,591
FILING DATE: 16-Apr-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US-09/489,770
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/966,317
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 16,749
REFERENCE/DOCKET NUMBER: PF-0403 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-955-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Linear
LIBRARY: GenBank
CLONE: 20419
SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-124-591-4

Query Match 42.8%; Score 349.5; DB 13; Length 146;
Best Local Similarity 47.2%; Pred. No. 2.3e-30;
Matches 68; Conservative 18; Mismatches 51; Indels 7; Gaps 3;

Qy 6 VLVFLCLVALVLTQFGMIEKMTGKSA-LQNDYGYCIGIGGSHRPVDQTD 59
Db 3 VLLLAIVMIAFGS1IQQGS1LEFQMLFKTGKRAVDSYGFYGCIGGSHRPVDQTD 62

Qy 7 LVFLCLVALVLTQFGMIEKMTGKSA-LQNDYGYCIGIGGSHRPVDQTDWCCHAH 65
Db 60 WCCHAIDCCYGRLEKLGCEPKLEKYLFSVSRGIFCA-GRITTCQRLTCECDKRALCFR 118
Db 63 WCCVTHACCTARLERGKGTFKLYKESYRGQ1QSNTDSCRQLQQCDKAEECFAR 122

Qy 119 NLGTYNRKYAHYPNKLCTGPTPPC 142
Db 123 NRKSYSLKQFYLNKESKGKTPSC 146

RESULT 11
 US-09-917-805-6
 Sequence 6, Application US/09917805
 Publication No. US20040073573A1.
 GENERAL INFORMATION:
 APPLICANT: STYNE, Sten
 APPLICANT: STAHL, Ulf
 APPLICANT: EK, Bo
 APPLICANT: SJODAHL, Staffan
 TITLE OF INVENTION: PLANT ENZYME AND USE THEREOF
 FILE REFERENCE: STYNE=1
 CURRENT APPLICATION NUMBER: US/09/917,805
 CURRENT FILING DATE: 2001-07-31
 PRIORITY NUMBER: 09/155,124
 PRIOR FILING DATE: 1999-03-02
 PRIORITY NUMBER: PCT/SE97/00554
 PRIOR FILING DATE: 1997-03-27
 PRIORITY NUMBER: 9601237.2
 PRIOR FILING DATE: 1996-03-29
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 6
 LENGTH: 138
 TYPE: PRT
 ORGANISM: Vipera ammodytes
 US-09-917-805-6

Query Match Score 325.5; DB 12; Length 138;
 Best Local Similarity 48.6%; Pred. No. 9.4e-28;
 Matches 67; Conservative 15; Mismatches 51; Indels 5; Gaps 4;

RESULT 13
 US-09-975-456B-9
 Sequence 9, Application US/09975456B
 Publication No. US20030073057A1
 GENERAL INFORMATION:
 APPLICANT: LAZDUNSKI, MICHEL
 APPLICANT: LAMBEAU, GERARD
 APPLICANT: VALENTIN, EMMANUEL
 TITLE OF INVENTION: NOVEL MAMMALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2
 FILE REFERENCE: 1478-R-00
 CURRENT APPLICATION NUMBER: US/09/975,456B
 CURRENT FILING DATE: 2002-08-27
 PRIORITY NUMBER: 60/239,491
 PRIOR FILING DATE: 2000-10-11
 NUMBER OF SEQ ID NOS: 10
 SEQ ID NO 9
 LENGTH: 138
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-975-456B-9

Query Match Score 317.5; DB 10; Length 138;
 Best Local Similarity 45.7%; Pred. No. 7.1e-27;
 Matches 59; Conservative 52; Mismatches 17; Indels 1; Gaps 1;

RESULT 12
 US-09-917-805-2
 Sequence 2, Application US/09917805
 Publication No. US20040073973A1
 GENERAL INFORMATION:
 APPLICANT: STYNE, Sten
 APPLICANT: STAHL, Ulf
 APPLICANT: EK, Bo
 APPLICANT: SJODAHL, Staffan
 TITLE OF INVENTION: PLANT ENZYME AND USE THEREOF
 FILE REFERENCE: STYNE=1
 CURRENT APPLICATION NUMBER: US/09/917,805
 CURRENT FILING DATE: 2001-07-31
 PRIORITY NUMBER: 09/155,124
 PRIOR FILING DATE: 1999-03-02
 PRIORITY NUMBER: PCT/SE97/00554
 PRIOR FILING DATE: 1997-03-27
 PRIORITY NUMBER: 9601237.2
 SEQ ID NO 2
 LENGTH: 138
 TYPE: PRT
 ORGANISM: Trimeresurus flavoviridis
 US-09-917-805-2

Query Match Score 39.9%; DB 12; Length 138;
 Best Local Similarity 48.6%; Pred. No. 9.4e-28;
 Matches 67; Conservative 15; Mismatches 51; Indels 5; Gaps 4;

RESULT 14
 US-09-969-384-17
 Sequence 17, Application US/09969384
 Publication No. US20020192749A1
 GENERAL INFORMATION:
 APPLICANT: Moore et al.
 TITLE OF INVENTION: Human Gene Polynucleotides, Polypeptides, and Antibodies
 FILE REFERENCE: PT055P1
 CURRENT FILING DATE: 2001-10-03
 PRIORITY NUMBER: PCT/US01/10542
 PRIOR FILING DATE: 2001-04-02
 PRIORITY NUMBER: 60/235,384
 PRIOR FILING DATE: 2000-09-29
 PRIORITY NUMBER: 60/194,118
 PRIOR FILING DATE: 2000-04-03
 NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 17
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-969-384-17

Query Match 31.0%; Score 310.5; DB 9; Length 145;
Best Local Similarity 39.2%; Pred. No. 4.5e-26;
Matches 56; Conservative 23; Mismatches 57; Indels 7; Gaps 3;
Matches 56; Conservative 23; Mismatches 57; Indels 7; Gaps 3;

Qy 7 LVFLCLLVAV-----VIGNIVQFVMIERMTGK-SALOYNDYCCYCGGSHWPVDOTDW 60
Db 3 LALLGGIVMVAGVPIQGGILNLINKMVKQYTGRMPILSYWPGCHGIGRRGPKDADW 62

Qy 61 CCHAHDCCYCRLEKLGCEPKLEYLFVSVERGIFCAGR-TTCORLTCECDRAALCFRRN 119
Db 63 CCQTHDCCYCRLEKLGCEPKLEYLFVSVERGIFCAGR-TTCORLTCECDRAALCFRRN 119

Qy 120 LGTYNRKTAHYHYPNLKLTGTPPC 142
Db 123 LDTIQKRLRFYWRPHCRGQTPGC 145

RESULT 15
US-09-975-456B-7
Sequence 7, Application US/09975456B
Publication No. US200301073087A1
GENERAL INFORMATION:
APPLICANT: LAZDINSKI, MICHEL
APPLICANT: LAMBEAU, GERARD
APPLICANT: VALENTIN, EMANUEL
TITLE OF INVENTION: NOVEL MAMMALIAN SECRETED GROUP I IF PHOSPHOLIPASE A2
FILE REFERENCE: 1478-R-00
CURRENT APPLICATION NUMBER: US/09/975,456B
CURRENT FILING DATE: 2002-08-27
PRIOR APPLICATION NUMBER: 60/239,491
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 2.1
SEQ ID NO: 7
LENGTH: 145
TYPE: PRT
ORGANISM: Homo sapiens
US-09-975-456B-7

Query Match 38.0%; Score 310.5; DB 10; Length 145;
Best Local Similarity 39.2%; Pred. No. 4.5e-26;
Matches 56; Conservative 23; Mismatches 57; Indels 7; Gaps 3;
Matches 56; Conservative 23; Mismatches 57; Indels 7; Gaps 3;

Qy 7 LVFLCLLVAV-----VIGNIVQFVMIERMTGK-SALOYNDYCCYCGGSHWPVDOTDW 60
Db 3 LALLGGIVMVAGVPIQGGILNLINKMVKQYTGRMPILSYWPGCHGIGRRGPKDADW 62

Qy 61 CCHAHDCCYCRLEKLGCEPKLEYLFVSVERGIFCAGR-TTCORLTCECDRAALCFRRN 119
Db 63 CCQTHDCCYCRLEKLGCEPKLEYLFVSVERGIFCAGR-TTCORLTCECDRAALCFRRN 119

Qy 120 LGTYNRKTAHYHYPNLKLTGTPPC 142
Db 123 LDTIQKRLRFYWRPHCRGQTPGC 145

Search completed: July 3, 2004, 05:27:05
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1	81.7	100.0	142	1	PA2E_HUMAN	Q9N7K7	homo sapien
2	79.9	86.8	142	1	PA2E_MOUSE	Q9el13	mus musculus
3	37.3	45.7	137	1	PA2N_VIPAA	P34180	vipera ammo
4	37.2	45.5	121	1	PA21_ERIMA	P24293	eristocophi
5	36.8	45.1	144	1	PA2A_HUMAN	P14555	homo sapien
6	359.5	44.0	146	1	PA2A_RAT	P14423	rattus norvegicus
7	358.5	43.9	120	1	PA2_GERCE	P21789	cerastes cerastes
8	358.5	43.9	138	1	PA2Y_TRIFL	P09777	trimeresurus
9	355.5	43.5	121	1	PA2_DABER	P81458	daboia russica
10	355	43.3	121	1	PA2_VIPAA	Q9y9j7	vipera palau
11	354	43.3	137	1	PA24_AKGHP	Q42187	agkistrodon
12	351.5	43.0	138	1	PA2W_TRIFL	P00626	vipera ammo
13	351.5	43.0	138	1	PA2A_VIPAA	P21407	vipera ammo
14	350	42.8	123	1	PA21_AKGHP	P25172	agkistrodon
15	350	42.8	146	1	PA2A_MOUSE	P21482	mus musculus
16	349.5	42.8	138	1	PA21_BOTJR	P45881	bothrops jararaca
17	348.5	42.7	138	1	PA26_TRIFL	P70088	trimeresurus
18	348.5	42.7	138	1	PA2B_VIPAA	P24424	vipera ammo
19	345.5	42.3	138	1	PA2A_VIPAA	P21407	vipera ammo
20	345.5	42.3	138	1	PA2C_VIPAA	Q81iy9	trimeresurus
21	341.5	41.8	138	1	PA2_TRIUE	P25264	trimeresurus
22	340.5	41.7	122	1	PA2A_TRIFL	P00622	bitis caudalis
23	340	41.6	121	1	PA2_BITCA	P20680	trimeresurus
24	339.5	41.6	122	1	PA2X_TRIFL	Q93147	trimeresurus
25	339.5	41.6	138	1	PA2P_TRIFL	Q42188	agkistrodon
26	338.5	41.4	122	1	PA29_AKGHP	P59265	trimeresurus
27	338.5	41.4	122	1	PA2B_TRIFL	Q91968	trimeresurus
28	338.5	41.4	138	1	PA22_TRIFL	Q90w39	trimeresurus
29	338.5	41.4	138	1	PA2A_TRIFL	P47711	cavia porcellus
30	336	41.1	145	1	PA2M_CAVPO	P24476	trimeresurus
31	333.5	40.8	138	1	PA21_TRIFL	P59171	echis ocellatus
32	333.5	40.8	138	1	PA25_ECHOC	P24294	eristocophis color
33	332.5	40.7	122	1	PA22_EHCO	P042192	agkistrodon
						P06859	trimeresurus
						P81480	trimeresurus
							ALIGNMENTS
							RESULT 1
							PA2E_HUMAN
							STANDARD;
							PRT;
							142 AA.
							SEQUENCE FROM N.A., AND CHARACTERIZATION.
							RP MEDLINE=2014878; PubMed=10681567;
							RA Suzuki N., Ishizaki J., Yokota Y., Higashino K., Ono T., Ikeda M.,
							RA Fujii N., Kawamoto K., Hanasaki K.,
							RT Structures, enzymatic properties, and expression of novel human and
							mouse secretory phospholipase A(2)s.";
							RL J. Biol. Chem. 275:5785-5793 (2000)
							CC -1- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
							acyl groups in 3-sn-phosphoglycerides. Has a preference for
							arachidonic-containing phospholipids.
							-1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
							acetylglycerophosphocholine + a fatty acid anion.
							CC -1- COFACTOR: Binds 1 calcium ion per subunit.
							CC -1- SUBCELLULAR LOCATION: Secreted
							-1- TISSUE SPECIFICITY: Restricted to the brain, heart, lung, and
							placenta.
							CC -1- SIMILARITY: Belongs to the phospholipase A2 family.
							CC This SWISS-PROT entry is copyright of BioInformatics and the EMBL Outstation -
							the European Bioinformatics Institute. There are no restrictions on its
							use by non-profit institutions as long as its content is in no way
							modified and this statement is not removed. Usage by and for commercial
							entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
							CC
							EMBL AF189279; AAF65411; -
							DR HSSP; P14550; 1 POD.
							DR GO; GO:0004624; F:secreted phospholipase A2 activity; TAS.
							DR PRODRON; PDD00303; PhospholipaseA2; 1.
							DR GO; GO:0006954; P:inflammatory response; TAS.
							DR PROSTATE; PS00119; PA2_ASP; FALSE_NEG.
							DR PROSTATE; PS00118; PA2_HIS; 1.
							KW Hydrolase; Lipid degradation; Signal; Calcium.
							FT SIGNAL; 19 POTENTIAL.
							FT CHAIN 20 142 GROUP III SECRETORY PHOSPHOLIPASE A2.

- Query Match Score 372; DB 1; Length 121;
 Best Local Similarity 45.5%; Pred. No. 1.5e-32;
 Matches 70; Conservative 8; Mismatches 42; Indels 4; Gaps 3;
- Qy 20 NLVQFGVMTKMTGKSA-LOYNDGCGYCIGGGSHWVQDQTDWCHAHDCCYGRLEXLGCE 78
 Db 1 NLYQGKMKTMGKSA-LOYNDGCGYCIGGGSHWVQDQTDWCHAHDCCYGRLEXLGCE 58 [5]
- Qy 79 PKLERYLETSERGIFCAGRTTCORLTGCFDKRAALCFPRNLGTYNKAYAHPNKLCTGP 138
 Db 59 PKLSTSYSSYTFQNGD1VCGDNACLRAVECDRVAAICGENLNLYDRKXQYDPSQCT-E 117 [6]
- Qy 139 TPPC 142
 Db 118 TEQC 121
-
- RESULT 5**
- PA2A_HUMAN STANDARD; PRT; 144 AA.
- AC P14555; Q9UCD2; DT 01-JAN-1990 (Rel. 1.3, Created)
 DT 01-APR-1990 (Rel. 1.4, Last sequence update)
 DT 15-MAR-2004 (Rel. 4.3, Last annotation update)
- DE Phospholipase A2, membrane associated precursor (EC 3.1.1.4)
 DE (Phosphatidylcholine 2-acetylhydrolase) (Group IIA phospholipase A2)
 DE (GLIC SP42) (Non-secretory phospholipase A2) (NPS-PLA2).
 GN PLA2A OR PLA2B OR RASP-A OR PLA2L.
 OS Homo sapiens (Human).
- OC Mammalia; Metazoa; Chordata; Craniata; Euteleostomi;
 OC Eutheria; Primates; Catarrhini; Hominoidea; Homo;
 OX NCBI_TaxID:9606; RN [1]
- RP SEQUENCE FROM N.A. RX
- RC TISSUE=Reumatoid arthritic synovial fluid; MEDLINE=9917433; PubMed=2926608; RA Seihama J.J., Pruzanski W., Vadas P., Plant S., Miller J.A., RA Kloss J., Johnson L.K.; RT "Cloning and recombinant expression of phospholipase A2 present in rheumatoid arthritic synovial fluid."; RL J. Biol. Chem. 264:5335-5338(1989). [2]
- RP SEQUENCE FROM N.A. RX
- RC TISSUE=Reumatoid arthritic synovial fluid; MEDLINE=9917433; PubMed=2926633; RA Kramer R.M., Hession C., Johansen B., Hayes G., McGray P., Chow E.P., RA Tizard R., Pepinsky R.B.; RT "Structure and properties of a human non-pancreatic phospholipase A2."; RT "Structure and properties of a secretable phospholipase A2 from human platelets."; RL J. Biol. Chem. 264:5768-5775(1989). [3]
- RN SEQUENCE FROM N.A. RP
- RC TISSUE=Prostate; MEDLINE=91050334; PubMed=2239446; RA Kramer R.M., Johansen B., Hession C., Pepinsky R.B.; RT "Structure and properties of a secretable phospholipase A2 from human platelets."; RL Adv. Exp. Med. Biol. 275:35-53(1990). [4]
- RN SEQUENCE FROM N.A. RP
- RC TISSUE=Prostate; MEDLINE=2238857; PubMed=12477932; RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schueler G.D., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K., RA Hopkins R.F., Jordan R., Moore T., Max S.I., Wang J., Hsieh F., RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L., RA Stapleton M., Soars M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., RA Brown M.J., Urdin T.B., Yoshihara S., Carmine P., Prange C., RA Raha S.S., Locqueur N.A., Peters G.J., Abramson R.D., Mullally S.J., RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia B.J., Lu X., Gibbs R.A., RA Villalon D.K., Muzny D.M., Sodergren E.B., Sato T., Ohtan M., Miki K., RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
- Whiting M., Madan A., Young A.C., Shvachchenko Y., Bouffard G.G., RA Rodriguez R.W., Touchman J.W., Grimes B.D., Dickson M.C., RA Rodriguez A.C., Grimwood J.J., Schnitzel J., Myers R.M., RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., RA Schniech A., Schein J.E., Jones S.J.M., Marra M.A.; RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; RT human and mouse cDNA sequences"; RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). RN [5]
- RP SEQUENCE OF 21-144. RX
- RC TISSUE=Spleen; MEDLINE=83734261; PubMed=2775276; RX
- RA "The primary structure of a membrane-associated phospholipase A2 from human spleen."; RT Biochem. Biophys. Res. Commun. 163:42-48(1989). RL [6]
- RP SEQUENCE OF 21-54. RX
- RC TISSUE=Synovial fluid; MEDLINE=89197814; PubMed=3240982; RX
- RA Hara S., Kudo I., Matsuta K., Miyamoto T., Inoue K., RA "Amino acid composition and NH2-terminal amino acid sequence of human phospholipase A2 purified from rheumatoid synovial fluid"; RT J. Biochem. 104:326-328(1988). RL [7]
- RP SEQUENCE OF 21-33. RX
- RC TISSUE=Synovial fluid; MEDLINE=89076274; PubMed=3202859; RX
- RA Lai C.Y., Wada K.; RT "Phospholipase A2 from human synovial fluid: purification and structural homology to the placental enzyme."; RL Biochem. Biophys. Res. Commun. 157:488-493(1988). RL [8]
- RP SEQUENCE OF 21-75. RX
- RC TISSUE=Ileal mucosa; MEDLINE=94002200; PubMed=8399335; RX
- RA Minami T., Tojo H., Shinomura Y., Matsuzawa Y., Okamoto M.; RT "Purification and characterization of a phospholipase A2 from human ileal mucosa."; RL Biochem. Biophys. Acta 1170:125-130(1993). RL [9]
- RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS). RX
- RA Wery J.-P., Schevitz R.W., Clawson D.K., Bobbitt J.L., Dow E.R., RA Gamboa G., Goodwin T.J.R., Hermann R.B., McClure D.B., RA Miheilich E.D., Putnam J.E., Sharp J.D., Stark D.H., Teater C., RA Warrick M.W., Jones N.D.; RT "Structure of recombinant human rheumatoid arthritic synovial fluid phospholipase A2 at 2-A resolution."; RL Nature 352:79-82(1991). RL [10]
- RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS). RX
- RA Scott D.L., White S.P., Browning J.L., Rosa J.J., Gelb M.H., RA Sigler P.B.; RT "Structures of free and inhibited human secretory phospholipase A2"; RT "Structure of recombinant human inflammatory exudate."; RL Science 254:1007-1010(1991). RL [11]
- RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS). RX
- RA Schevitz R.W., Bach N.J., Clawson D.G., Chirgadze N.Y., Clawson D.K., RA Dillard R.D., Draheim S.E., Hartley L.W., Jones N.D., Michelich E.D., RA Olkowski J.L., Snyder D.W., Dand S.C., Wery J.-P.; RT "Structure-based design of the first potent and selective inhibitor of human non-pancratic secretory phospholipase A2.," RT Nat. Struct. Biol. 2:458-465(1995). RL [12]
- RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS). RX
- RA Kitaddoro K., Hagi-shira S., Sato T., Ohtan M., Miki K.; RT "Crystal structure of human secretory phospholipase A2-IIA complex with the potent indolizine inhibitor 120-1032.," RT

	FT	TURN	127	128
BL	J. Biochem.	123:619-623(1998)		
CC	-!	FUNCTION: Thought to participate in the regulation of the phospholipid metabolism in biomembranes including eicosanoid biosynthesis. Catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerol.		
CC	-!	CATALYTIC ACTIVITY: Phosphatidylcholine + H ₂ O = 1-acyl glycerophosphocholine + a fatty acid anion.		
CC	-!	COPARTNER: Binds 1 calcium ion per subunit.		
CC	-!	SUBCELLULAR LOCATION: Membrane-associated.		
CC	-!	MISCELLANEOUS: Group II phospholipase A2 is found in many cells and also extracellularly. The membrane-bound and secreted forms are identical and are encoded by a single gene.		
CC	-!	SIMILARITY: Belongs to the phospholipase A2 family.		
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).		
CC		-----		
DR	EMBL; M22430; AAA3550_1;			
DR	EMBL; M22431; AAA3549_1;			
DR	EMBL; BC00591_1;			
DR	PIR; A32862; PSHYTF.			
DR	PDB; 1AYP; 1AYP; 31-JUL-95.			
DR	PDB; 1POD; 1POD; 31-OCT-93.			
DR	PDB; 1POE; 1POE; 31-OCT-93.			
DR	PDB; 1KYO; 1KYO; 07-JUL-97.			
DR	PDB; 1DB4; 1DB4; 12-NOV-99.			
DR	PDB; 1DB5; 1DB5; 12-NOV-99.			
DR	PDB; 1DCY; 1DCY; 12-NOV-99.			
DR	Genew; HGNC:9031; PLA2G2A.			
DR	MIM; 172411; -.			
DR	GO; GO:0004623; E:phospholipase A2 activity; TAS.			
DR	InterPro; IPR001211; PhospholipaseA2.			
DR	IPR00683; phospholipaseA2.			
DR	PRINTS; PR00389; PHPLIPASEA2.			
DR	PRODOM; PD000303; PhospholipaseA2 ; 1.			
DR	SMART; SM00083; PAZC; 1.			
DR	PROSITE; PS000118; PA2_HIS; 1..			
DR	PROSITE; PS000119; PA2_ASPI; 1..			
KW	KW3-structure: Lipid degradation; Membrane; Signal; Calcium; 3D-structure.			
FT	SIGNAL	1	20	PHOSPHOLIPASE A ₂ , MEMBRANE ASSOCIATED.
FT	CHAIN	21	144	BY SIMILARITY.
FT	ACT SITE	67	67	BY SIMILARITY.
FT	ACT SITE	111	111	BY SIMILARITY.
FT	DISULFID	46	137	
FT	DISULFID	48	64	
FT	DISULFID	63	117	
FT	DISULFID	69	144	
FT	DISULFID	70	110	
FT	DISULFID	79	103	
FT	DISULFID	97	108	
FT	METAL	47	47	CALCIUM (VIA CARBONYL OXYGEN).
FT	METAL	49	49	CALCIUM (VIA CARBONYL OXYGEN).
FT	METAL	51	51	CALCIUM (VIA CARBONYL OXYGEN).
FT	METAL	68	68	CALCIUM.
FT	HELIX	22	33	
FT	HELIX	37	40	
FT	TURN	41	41	
FT	TURN	45	47	
FT	HELIX	59	75	SEQUENCE FROM N.A.
FT	TURN	76	78	RC STRAIN=Sprague-Dawley; TISSUE=Platelet;
FT	STRAND	88	91	RX MEDLINE=89174508; PubMed=3235451;
FT	TURN	92	93	RA Hayakawa M., Kudo I., Tomita M., Nojima S., Inoue K.;
FT	STRAND	94	97	RT "The primary structure of rat platelet phospholipase A2.";
FT	HELIX	102	102	RL J. Biochem. 104:767-772(1988).
FT	TURN	121	121	RN SEQUENCE OF 22-57.
FT	HELIX	122	124	RC

	FT	TURN	127	128
QY	12	LIVALT-----	45-18;	Score 368.5; DB 1; Length 144;
QY	12	GNLVQGVMIKMGT-SALQNDYCGYCGGSHMPVDQTDWCC	Best Local Similarity 52.11;	Pred. No. 4.3e-12;
Db	5	LLAVMNFGLIQAHHVNFRMILKTGGTEAALSYYGPVGCCHGGRGSPKDAFDRCC	Matches 73;	Indels 9; Gaps 2;
QY	63	HHDCCYGRLEKLGEPKLEYLFSVSEFGCAAGTCQLTCEDDKRALCPNLGT	Conservative 12;	Mismatches 46;
Db	65	VTHDCCYKRLERKGCKFLSYKFNSNSRITCAKODDSQRSQCECDKAATCPARNKTT		124
RESULT 6				
PA2A_RAT	ID	PA2A_RAT	STANDARD:	PRT; 146 AA.
AC	AC	P2A23;		
DT	DT	01-JAN-1990 (Rel. 13, Created)		
DT	DT	01-FEB-1991 (Rel. 17, Last sequence update)		
DT	DT	15-MAR-2004 (Rel. 43, Last annotation update)		
DE	DE	Phospholipase A2, membrane associated precursor (EC 3.1.1.4)		
DE	DE	(Phosphatidylcholine 2-acetylhydrolase) (Group IIIA phospholipase A2)		
GN	GN	PLA2G2A.		
OS	OS	Rattus norvegicus (Rat).		
OC	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Rattus.		
OX	OX	NCBI_TaxID=10116;		
RN	RN	[1]		
RP	RP	SEQUENCE FROM N.A.		
RC	RC	STRAIN=Sprague-Dawley; TISSUE=Platelet;		
RX	RX	MEDLINE=90110033; PubMed=2606307;		
RA	RA	Komada M., Kudo I., Mizushima H., Kitamura N., Inoue K.;		
RA	RA	"Structure of cDNA coding for rat platelet phospholipase A2."		
RL	RL	J. Biochem. 106:545-547(1989).		
RN	RN	[2]		
RP	RP	SEQUENCE FROM N.A.		
RC	RC	TISSUE=Spleen;		
RX	RX	MEDLINE=90167443; PubMed=2346480;		
RA	RA	Komada M., Kudo I., Inoue K.;		
RT	RT	"Structure of gene coding for rat group II phospholipase A2."		
RL	RL	Biochem. Biophys. Res. Commun. 168:1059-1065(1990).		
RP	RP	SEQUENCE FROM N.A.		
RX	RX	MEDLINE=89150938; PubMed=2764915;		
RA	RA	Ishizaki J., Ohara O., Nakamura E., Tamaki M., Ono T., Kanda A.;		
RA	RA	Yoshida N., Teraiwa H., Tojo H., Okamoto M.;		
RA	RA	"cDNA cloning and sequence determination of rat membrane-associated phospholipase A2."		
RT	RT	Biochem. Biophys. Res. Commun. 162:1030-1036(1989).		
RL	RL	[4]		
RP	RP	SEQUENCE FROM N.A.		
RC	RC	STRAIN=Wistar, TISSUE=Platelet;		
RX	RX	MEDLINE=90181322; PubMed=12400792;		
RA	RA	Kusunoki C., Sato S., Kobayashi M., Niwa M.;		
RA	RA	"Structure of genomic DNA for rat platelet phospholipase A2."		
RL	RL	J. Biochem. 104:767-772(1988).		
RN	RN	[5]		
RP	RP	SEQUENCE OF 22-146.		
RC	RC	STRAIN=Wistar, TISSUE=Platelet;		
RX	RX	MEDLINE=89174508; PubMed=3235451;		
RA	RA	Hayakawa M., Kudo I., Tomita M., Nojima S., Inoue K.;		
RT	RT	"The primary structure of rat platelet phospholipase A2."		
RL	RL	J. Biochem. 104:767-772(1988).		
RN	RN	[6]		
RP	RP	SEQUENCE OF 22-57.		
RC	RC			

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 CC or send an email to license@isb-sib.ch).

DR EMBL; AB07213; BAB6546; 1.
 DR InterPro; IER01211; PhospholipaseA2.
 DR Pfam; PF00068; PhospholipaseA2.
 DR PRINTS; PR00389; PHOSPHOLIPASEA2.
 DR PRODOM; PD000303; PhospholipaseA2; 1.
 DR SMART; SM0085; PA2; 1.
 DR PROSITE; PS00119; PA2 ASP; 1.
 DR PROSITE; PS00118; PA2 HIS; 1.
 DR Hydrolease; Lipid degradation; Calcium; Multigene family; Signal;
 KW Calcium; Multigene family; Signal.
 ACT SITE 47 BY SIMILARITY.
 ACT SITE 89 BY SIMILARITY.
 DISULFID 26 115 BY SIMILARITY.
 DISULFID 28 44 BY SIMILARITY.
 DISULFID 43 95 BY SIMILARITY.
 DISULFID 50 88 BY SIMILARITY.
 DISULFID 57 81 BY SIMILARITY.
 FT DISULFID 75 86 BY SIMILARITY.
 METAL 27 27 CALCIUM (VIA CARBONYL OXYGEN)
 METAL 29 29 CALCIUM (VIA CARBONYL OXYGEN)
 METAL 31 31 CALCIUM (VIA CARBONYL OXYGEN)
 METAL 48 48 CALCIUM (BY SIMILARITY).
 FT VARIANT 10 12 FKM -> KHK (IN STRAIN TUNISIA).
 FT VARIANT 17 19 PIF -> ALL (IN STRAIN TUNISIA).
 FT VARIANT 22 23 GD -> SA (IN STRAIN TUNISIA).
 SQ SEQUENCE 120 AA; 13534 MW; E681FA/001662C3 CRC64;
 Query Match 43.9%; Score 358.5; DB 1; Length 120;
 Best Local Similarity 54.2%; Pred. No. 4.2e-31;
 Matches 64; Conservative 10; Mismatches 41; Indels 3; Gaps 2;
 Qy 20 NLVQFGKMLPKMTGKSPISFYGCVGGKGKTPVDATDRCCFVHDCGYGRVN--SCN 58
 Ddb 1 NLYQFGKMLPKMTGKSPISFYGCVGGKGKTPVDATDRCCFVHDCGYGRVN--SCN 58
 Qy 79 PKLEYTFLYSVERGIFCAERTTCACTTCACTTCRLLCRAVCECDRVIAFCPEVNITYDKKKDPTSQCT 136
 Ddb 59 PKRSTVSYSPQNGGIVCDONLCKRAVCECDRVIAFCPEVNITYDKKKDPTSQCT 116
 RESULT 9
 PA2Q TRIFL STANDARD; PRT; 138 AA.
 Q90Y77; 28-FEB-2003 (Rel. 41, Created)
 "Regional evolution of Trimeresurus flavoviridis venom-gland phospholipase A2 isozyymes."
 Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides (By similarity).
 CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerophosphocholine + a fatty acid anion.
 COFACTOR: Binds 1 calcium ion per subunit (By similarity).
 SUBCELLULAR LOCATION: Secreted (By similarity).
 TISSUE SPECIFICITY: Expressed by the venom gland (Probable).
 SIMILARITY: Belongs to the phospholipase A2 family. Group II subfamily.

SEQUENCE FROM N.A.
 Chijiwa T., Yamaguchi Y.; Ogawa T.; Deshimaru M.; Nobuhisa I., Nakashima K.-I., Oda-Ueda N., Shimohigashi Y., Fukumaki Y., Hattori S., Ohno M.;
 "Regional evolution of Trimeresurus flavoviridis venom-gland phospholipase A2 isozyymes."
 Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides (By similarity).
 CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerophosphocholine + a fatty acid anion.
 COFACTOR: Binds 1 calcium ion per subunit (By similarity).
 SUBCELLULAR LOCATION: Secreted (By similarity).
 TISSUE SPECIFICITY: Belongs to the phospholipase A2 family. Group II subfamily.

SEQUENCE FROM N.A.
 STRAIN=Amani-Oshima, and Kagoshima; TISSUE=Venom gland;
 ID PA2Q TRIFL STANDARD; PRT; 138 AA.
 AC Q8JTG0; DT 28-FEB-2003 (Rel. 41, Created)
 Db 4 LWMATVLYVGVEGHQLFRKMTKEPIVSYAVGCGKGRGKPKXDATDRCCFVH 63
 Qy 66 DCYCGRGLERLGEPKLKEYLVSERGIFCAGRTTTCRLTCGDKAALCPRRNLTYNR 125
 Db 64 DCYCERYV-TGCDPKNDYYTTSLENGDIVCGGDNPCTKVCECDKAAACFPRDNLYTKK 121
 Qy 126 KYAHYPNKLCTGPTPPC 142
 Db 122 RIMTFPDIFFCTDTEC 138
 RN NCBI_TaxID:88087; RP SEQUENCE FROM N.A.
 RC STRAIN=Amani-Oshima, and Kagoshima; TISSUE=Venom gland;
 RX DT 28-FEB-2003 (Rel. 41, Last sequence update)
 RA Chijiwa T., Yamaguchi Y.; Ogawa T.; Deshimaru M.; Nobuhisa I., Nakashima K.-I., Oda-Ueda N.; Fukumaki Y., Hattori S., Ohno M.; PA RT "Interisland evolution of Trimeresurus flavoviridis."
 OC Lepidosaurs; Metatoa; Chordata; Craniata; Vertebrata; Buteleostomi; OC Crotalinae; Viperidae; Crotalinae; Trimeresurus.
 OC NCBI_TaxID:88087; OX RESULT 8
 PA2Q TRIFL STANDARD; PRT; 138 AA.
 ID PA2Q TRIFL STANDARD; PRT; 138 AA.
 AC Q8JTG0; DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DI Phospholipase A2 isozyme CPLA-B, (A) precursor (EC 3.1.1.4)
 DE (Phosphatidylcholine 2-acetylhydrolase).
 OS Trimeresurus flavoviridis (Habu).
 OC Eukaryota; Metatoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Lepidosaurs; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Trimeresurus.
 OX NCBI_TaxID:88087;
 RN SEQUENCE FROM N.A.
 RA Chijiwa T., Yamaguchi Y.; Ogawa T.; Deshimaru M.; Nobuhisa I., Nakashima K.-I., Oda-Ueda N., Shimohigashi Y., Fukumaki Y., Hattori S., Ohno M.;
 CC "Regional evolution of Trimeresurus flavoviridis venom-gland phospholipase A2 isozyymes."
 CC Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides (By similarity).
 CC CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerophosphocholine + a fatty acid anion.
 CC COFACTOR: Binds 1 calcium ion per subunit (By similarity).
 CC SUBCELLULAR LOCATION: Secreted (By similarity).
 CC TISSUE SPECIFICITY: Belongs to the phospholipase A2 family. Group II subfamily.

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RL J. Mol. Evol. 56:286-293 (2003).
 CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the
 CC 2-acyl groups in 3-sn-phosphoglycerides.
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 acylglycerophosphocholine + a fatty acid anion.
 CC -!- COPARTNER: Binds 1 calcium per subunit (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- SIMILARITY: Belongs to the phospholipase A2 family. Group II
 subfamily.

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EMBL; AB087498; BRC02719.1;
 InterPro; IPR012121; PhospholipaseA2.
 Pfam; PF00068; phospholipaseA2.
 PRINTS; PR00389; PHOSPHOLIPASEA2.
 ProDom; PD000403; PhospholipaseA2; 1.
 SMART; SMC0085; PA2c; 1.
 PROSITE; PS00119; PA2-ISP; 1.
 DR PROSITE; PS00118; PA2-HIS; 1.
 KW Hydrolase; Lipid degradation; Calcium; Multigene family; Signal.
 FT SIGNAL 16 BY SIMILARITY.
 FT CHAIN 17 138 PHOSPHOLIPASE A2 ISOZYME CPLA-B (A).
 FT ACT SITE 63 63 BY SIMILARITY.
 FT ACT SITE 105 105 BY SIMILARITY.
 FT DISULFID 42 131 BY SIMILARITY.
 FT DISULFID 44 60 BY SIMILARITY.
 FT DISULFID 59 111 BY SIMILARITY.
 FT DISULFID 65 138 BY SIMILARITY.
 FT DISULFID 66 104 BY SIMILARITY.
 FT DISULFID 73 97 BY SIMILARITY.
 FT DISULFID 91 102 BY SIMILARITY.
 FT METAL 43 43 BY SIMILARITY.
 FT METAL 45 45 BY SIMILARITY.
 FT METAL 47 47 BY SIMILARITY.
 FT METAL 64 64 CALCIUM (BY SIMILARITY).
 SQ SEQUENCE 138 AA; 15703 MW; CEDE54051DD2F10 CRC44;

Query Match 43.5%; Score 355.5; Length 138;
 Best local Similarity 49.2%; Pred. No. 1e-30; Indels 4; Gaps 2;
 Matches 65; Conservative 17; Mismatches 41; Strands 3;

Qy 12 LIVALYTGNIYQFGVMIKETGKSAQ-QNDYGGCXYGIGGSRSHRPVQDTDWCCCHAHDCCYG 70
 :|:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 Db 9 VLLVEGVHQLQFRMVKTCGKPEPIVSTAFYGYCGKGGRPKDAIDRCCEVHDCCYG 68
 ::-||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 Qy 71 RLEKKGCPFLERFLSVERGICAGRTTCQBLITCECDPRAALCPRNLYKPNRKYAH 130
 ::-||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 Db 69 KV--TGCDPFDWYDYZTSSSENGDIVCEGDNPCTKEVCECDKAIAACFRDLNLYKCRYMF 126
 ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 Qy 131 PNKLCTGPTPC 142
 :||:||:||:||:
 Db 127 PDIRCTDPFKC 138

RESULT 10
 PA2_DABRR STANDARD PRT: 121 AA.
 AC P81158;
 ID PA2_DABRR
 DB 15-DBC-1998 (Rel. 37, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Phospholipase A2 RVV-VD (EC 3.1.1.4) (Phosphatidylcholine 2-

DE acylhydrolase).
 OS Daboia russelli russelli (Russell's viper) (Vipera russelli russelli).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Leptosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Viperinae; Daboia.
 OC NCBI_TaxID=31159;
 RN [1];
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RC TISSUE=Venom;
 RX MEDLINE=98267643; PubMed=9604284;
 RA Carretero B.; Westerlund B.; Persson B.; Saarinen M.; Ranaswamy S.; Baker D.; Ekblad H.;
 RT "The three-dimensional structures of two toxins from snake venom throw light on the anticoagulant and neurotoxic sites of phospholipase A2".
 RT Toxicon 36:75-92 (1998).
 -: FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides. This protein has
 CC acyl groups in 3-sn-phosphoglycerides. This protein has
 CC anticoagulant activity.
 CC CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerophosphocholine + a fatty acid anion.
 CC -!- COFACTOR: Binds 1 calcium ion per subunit.
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the phospholipase A2 family. Group II subfamily.
 CC PDB; 1V1P; 1E-JUN-37.
 DR InterPro; IPR01211; PhospholipaseA2.
 DR Pfam; PF00068; Phoslip; 1.
 DR PRINTS; PR00389; PHOSPHOLIPASEA2.
 DR ProDom; PD000403; PhospholipaseA2; 1.
 DR SMART; SM00085; PA2c; 1.
 DR PROSITE; PS00119; PA2-ASP; 1.
 DR PROSITE; PS00118; PA2-HIS; 1.
 RW Hydrolase; Lipid degradation; Calcium; 3D-structure.
 FT ACT SITE 47
 FT ACT SITE 89
 FT DISULFID 26 115
 FT DISULFID 28 44
 FT DISULFID 43 95
 FT DISULFID 49 121
 FT DISULFID 50 88
 FT DISULFID 57 81
 FT DISULFID 75 86
 FT METAL 27 27
 FT METAL 29 29
 FT METAL 31 31
 FT METAL 48 48
 FT METAL 54 54
 FT METAL 55 57
 FT METAL 59 61
 FT METAL 66 68
 FT METAL 73 75
 FT METAL 80 98
 FT TURN 99 102
 FT HELIX 105 107
 FT STRAND 108 108
 FT TURN 109 109
 FT HELIX 112 114
 SQ SEQUENCE 121 AA; 13626 MW; 98CBC4A8922A89D1 CRC64;
 Query Match 43.5%; Score 355; DB 1; Length 121;
 Best Local Similarity 53.2%; Pred. No. 9.9e-31;
 Matches 66; Conservative 13; Mismatches 41; Indels 4; Gaps 3;

20	NLVQFGNMIEKMTGKSAL-QYNDYGCYCGIGGSHWPVTDWCHAHDCYGRLEKUGCE	43.3%	Score 354; DB 1;	Length 137;
21	NUFQFAENTVKTGKGPNLPSYDGYCIGWGSGKGPQDATDRCCFVHDCCYEVVK--	54.5%	Pred. No. 1.4e-30;	Best Local Similarity
Db	58	Matches 66; Conservative Matches 66; Mismatches 11;	Indels 4;	Gaps 2;
22	79 PKEKYLEFSVERGIFCAGRITTCQRLTCECDRKAALCFPRNLTGYNRAHYPNKLCTGP	138	7 LVFLCLIVLVALTGNYLQFGNMIEKMTGKSAL-QYNDYGCYCGIGGSHWPVTDWCHAHDC	66
Db	59 PKLSLYSFSQNGGIVVCDDNHSCKRAVECDRVAATCFRDNLNTYDKKXHNPSPSQCTG-	117	6 IAVVCLIG--VEGNLQFGNMIFPKRKSALSYSQDGCYCGMGGRKGPQDATDRCCFVHD	63
23	139 TPPC 142	67 CCYGRALKLGCPKLEYLFVSVERGIFCAGRITTCQRLTCECDRKAALCFPRNLTGYNRAH	126	
Db	118 TEQC 121	64 CCYGRVN--GCDPKLSTVSYSSQNGGIVCGDDPCRAVCECDRVAACFGENMNTYDTK	121	
<hr/>				
RESULT 11				
24	PA28_VIPPA	STANDARD;	PRT;	137 AA.
AC	Q9YGJ7;			
DT	28-FEB-2003	(Rel. 41, Created)		
DE	28-FEB-2003	(Rel. 41, Last sequence update)		
DS	Phospholipase A2 homolog VP8 precursor.			
DC	vipera Palaeastinae (Palestine viper) (Pseudocerastes palaestinae).			
DC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
DC	Lepidosauroidea; Squamata; Scincidae; Serpentes; Colubroidea;			
DC	Viperidae; Viperinae; Vipera.			
NCBI_TAXID	=48068;			
[1]	SEQUENCE FROM N.A.			
TISSUE_LIVER;	SEQUENCE FROM N.A.			
AC	MEDLINE=99011427; PubMed=9792822;			
AC	Kordis D., Bodelin A., Gubens F.;			
AC	"Positive darwinian selection in Vipera palaestinae phospholipase A2 genes is unexpectedly limited to the third exon."			
RT	Biochem. Biophys. Res. Commun. 251:613-619(1998).			
DL	-!- FUNCTION: Is not toxic by itself, but the synergistical mixture of			
DC	VIP7 and VP8 is lethal to mice (By similarity).			
DC	-!- SUBUNIT: Does not form a complex (By similarity).			
DC	-!- TISSUE_SPECIFICITY: Secreted (By similarity).			
DC	-!- SIMILARITY: Belongs to the phospholipase A2 family. Group II subfamily.			
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CC	EMBL; AF091854; AAC78084.1;			
CC	HSSP; P81458; 1VTF.			
CC	InterPro; IPR001211; PhospholipaseA2.			
CC	DR Pfam; PF00068; phosphlipase_1.			
CC	PRINTS; PR00389; PHOSPHOLIPASEA2.			
CC	PRODom; PD000303; PhospholipaseA2.			
CC	SMART; SM00085; PA2C_1.			
CC	PROSITE; PS00119; PA2 ASP; 1.			
CC	PROSITE; PS00118; PA2 HIS; 1.			
CC	Toxin; Signal; Multigene family.			
CC	SIGNAL; 16 BY SIMILARITY.			
CC	PHOSPHOLIPASE A2 HOMOLOG VP8.			
CC	DR ACT SITE 62 62 BY SIMILARITY.			
CC	ACT SITE 104 104 BY SIMILARITY.			
CC	DISULFID 41 130 BY SIMILARITY.			
CC	DISULFID 43 59 BY SIMILARITY.			
CC	DISULFID 58 110 BY SIMILARITY.			
CC	DISULFID 64 137 BY SIMILARITY.			
CC	DISULFID 65 103 BY SIMILARITY.			
CC	DISULFID 72 96 BY SIMILARITY.			
CC	DISULFID 90 101 BY SIMILARITY.			
CC	SEQUENCE 137 AA; 15349 MW; 281ACB6F82103D9 CRG64;			
CC	BY SIMILARITY.			
CC	FT PHOSPHOLIPASE A2 B.			
CC	FT CHAIN 17 137 BY SIMILARITY.			
CC	FT CHAIN 17 137 BY SIMILARITY.			
CC	DR PIR; JC13421; JC1342.			
CC	DR PDB; 1B4W; 12-JUN-98.			
CC	DR InterPro; IPR01211; PhospholipaseA2.			
CC	DR Pfam; PF00068; Phoslipase_1.			
CC	DR PRINTS; PR00389; PHOSPHOLIPASEA2.			
CC	DR PRODom; PD000303; PhospholipaseA2.			
CC	DR SMART; SM00085; PA2C_1.			
CC	DR PROSITE; PS00119; PA2 ASP; 1.			
CC	DR PROSITE; PS00118; PA2 HIS; 1.			
CC	DR KW Lipid degradation; Hydrolase; Signal; Calcium; Multigene family; 3D-structure.			
CC	FT SIGNAL 1 16 BY SIMILARITY.			
CC	FT CHAIN 17 138 BY SIMILARITY.			

ACT SITE		63	63	BY SIMILARITY.
ACT SITE		105	105	BY SIMILARITY.
DISULFID		42	131	BY SIMILARITY.
DISULFID		44	60	BY SIMILARITY.
DISULFID		59	111	BY SIMILARITY.
DISULFID		65	138	BY SIMILARITY.
DISULFID		66	104	BY SIMILARITY.
DISULFID		73	97	BY SIMILARITY.
DISULFID		91	102	BY SIMILARITY.
METAL		43	43	CALCIUM (VIA CARBONYL OXYGEN)
METAL		45	45	CALCIUM (VIA CARBONYL OXYGEN)
METAL		47	47	(BY SIMILARITY).
METAL		64	64	CALCIUM (VIA CARBONYL OXYGEN)
SEQUENCE		138 AA;	15614 MW;	149D21704F4AA437 CRC64;
Query Match Score 351.5%; DB 1; Length 138;				
Best Local Similarity 43.0%; Pred. No. 2.6e-30; Mismatches - 50; Indels 3; Gaps 2;				
Matches 66; Conservative 18; Mismatches - 50;				
7 LVFLCLLVAVLTGNLUQFGMIEKMTGKS ALQNYNDYGVCGTGGSHWPVDQIDWCCHHH 65				
4 LWIYAVLLVGEGSLLQPKMKMTGKEPPVVSAYFYCYCGSGGRGKPKDATDRCCFH 63				
66 DCCYGRLELKGCPEKLYTLFSVERGIAGRTICQRLTCEDDKRAALCFRRNLGTYNR 125				
64 DCCYEXL--TGCDPKWDYTYSWNGNTIVGGDDPCKKEVCEDKAAACFRDLNLTYYKK 121				
126 KYAHYPNKLCTGPPPPC 142				
122 RYMTYPNLIQSSKSEKC 138				
[1] NCBI_TaxID=88087;				
SEQUENCE FROM N.A.				
TISSUE=Venom gland				
MEDLINE=12409555; PubMed=1528861;				
Ogawa T., Oda N., Nakashima K.-I., Sasaki H., Hattori M., Sakaki Y.,				
Kihara H., Ohno M.,				
"Unusually high conservation of untranslated sequences in cDNAs for				
Trimeresurus flavoviridis phospholipase A2 isoforms."				
Proc. Natl. Acad. Sci. U.S.A. 89:8557-8561 (1992).				
(Phospholipid choline 2-acetylhydrolase).				
Trimeresurus flavoviridis (Babu).				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;				
Lepidosauria; Squamata; Sceloproglossa; Serpentes; Colubroidea;				
Viperidae; Crotalinae; Trimeresurus.				
[1] NCBI_TaxID=88087;				
SEQUENCE FROM N.A.				
PA2N_TRIPL STANDARD; PRT; 138 AA.				
Q02517; 01-FEB-1994 (Rel. 28, Created)				
01-FEB-1994 (Rel. 28, Last sequence update)				
10-OCT-2003 (Rel. 42, Last annotation update)				
Phospholipase A2 isozyme PL-X, precursor (EC 3.1.1.4)				
(Phospholipid choline 2-acetylhydrolase).				
-!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the				
2-acyl groups in 3-sn-phosphoglycerides.				
-!- CATALYTIC ACTIVITY: Phosphatidylcholine + H ₂ O = 1-				
acylglycerophosphocholine + a fatty acid anion.				
-!- COPACTOR: Binds 1 calcium ion per subunit (By similarity).				
-!- SUBCELLULAR LOCATION: Secreted.				
-!- TISSUE SPECIFICITY: Expressed by the venom gland.				
-!- SIMILARITY: Belongs to the phospholipase A2 family. Group II subfamily.				
RESULT 14				
PA2I_AGPPI STANDARD; PRT; 123 AA.				
ID PA2I_AGPPI AC P51972; DT 01-OCT-1996 (Rel. 34, Created)				
4 LWNIAVLLVGEGSLLQPKMKMTGKEPPVVSAYFYCYCGSGGRGKPKDATDRCCFH 63				
66 DCCYGRLELKGCPEKLYTLFSVERGIAGRTICQRLTCEDDKRAALCFRRNLGTYNR 125				
64 DCCYEVK--TGCDPKWDYTYSWNGNTIVGGDDPCKKEVCEDKAAACFRDLNLTYYKK 121				
DE (APP-D-19).				
Agkistrodon piscivorus piscivorus (Eastern cottonmouth)				
Eulipotyphla; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC Lepidosauria; Squamata; Sceloproglossa; Serpentes; Colubroidea;				
OC Viperidae; Crotalinae; Agkistrodon.				
NCBI_TaxID=8716;				
RN SEQUENCE.				
RC TISSUE=Venom				
RX MEDLINE=93257049; PubMed=8499705/				
RA Welch W., Reardon J.M., Heinrichs R.L.;				
RT An examination of structural interactions presumed to be of				
RT importance in the stabilization of phospholipase A2 dimers based upon				
RT comparative protein sequence analysis of a monomeric and dimeric				
RT enzyme from the venom of Agkistrodon D. piscivorus."				
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the European Bioinformatics Institute. There are no restrictions on its				
use by non-profit institutions as long as its content is in no way				
modified and this statement is not removed.				
Reviewed by and for commercial				

RL	J. Protein Chem. 12:187-193 (1993).	FT	TURN	70	71
RP	SEQUENCE OF 1-23, AND ACYLATION.	FT	STRAND	72	75
RC	TISSUE=Venom;	FT	HELIX	80	98
MDLNB=88298768; PubMed=3403524;		FT	TURN	99	99
RX	Cho W., Tomasselli A.G., Henrikson R.L., Kezdy F.J.;	FT	HELIX	100	102
RA	"The chemical basis for interfacial activation of monomeric phospholipases A2. Autochalytic derivatization of the enzyme by acyl transfer from substrate."	FT	STRAND	105	108
RT	J. Biol. Chem. 263:11237-11241(1988).	FT	TURN	109	109
RT	[3]	FT	HELIX	110	110
RT	CHARACTERIZATION.	FT	HELIX	113	116
RP	CHARACTERIZATION.	SQ	SEQUENCE	123 AA;	13989 MW;
RC	TISSUE=Venom;			C3986552D990D72	CRC64;
RX	MDLNB=8505416; PubMed=6438084;				
RA	Marignani J.M., Merutka G., Cho W., Welches W., Kezdy F.J., Heinriksson R.L.;				
RT	"A new class of phospholipases A2 with lysine in place of aspartate 49. Functional consequences for calcium and substrate binding.";				
RT	J. Biol. Chem. 259:13839-13843 (1984).				
RN	[4]				
RP	X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS);				
RC	TISSUE=Venom;				
RX	Medline=97166209; PubMed=9013608;				
RA	Han S.K., Yoon E.T., Scott D.L., Sigler P.B., Cho W.;				
RT	"Structural aspects of interfacial adsorption. A crystallographic and site-directed mutagenesis study of the phospholipase A2 from the venom of <i>Agkistrodon piscivorus piscivorus</i> .";				
RT	J. Biol. Chem. 272:3573-3582(1997).				
CC	-I- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2'-acyl groups in 3-sn-phosphoglycerides.				
CC	-I- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerophosphocholine + a fatty acid anion.				
CC	* -I- COPARTNER: Binds 1 calcium ion per subunit.				
CC	-I- SUBCELLULAR LOCATION: Secreted.				
CC	-I- PTM: Acylation causes dimerization.				
CC	-I- SIMILARITY: Belongs to the phospholipase A2 family. Group II subfamily. B53872. B53872;				
DR	PDB; 1VA8; 07-JUL-97.				
DR	InterPro; IPR01211; PhospholipaseA2.				
DR	Pfam; PF00068; phospholipaseA2.				
DR	PRINTS; PRO389; PHAPHLIPASEA2.				
DR	ProDom; PD000303; PhospholipaseA2; 1.				
DR	SMART; SM00085; PA2C; 1.				
DR	PROSITE; PS000119; PA2-ASP; 1.				
DR	PROSITE; PS000118; PA2-HIS; 1.				
KW	Hydrolase; Lipid degradation; Calcium; Lipoprotein; Palmitate;				
KW	3D-structure.	ACT SITE	47	BY SIMILARITY.	
FT		ACT SITE	89	BY SIMILARITY.	
FT		DISTSFID	26	116	
FT		DISTSFID	28	44	
FT		DISTSFID	43	95	
FT		DISTSFID	49	123	
FT		DISTSFID	50	88	
FT		DISTSFID	57	81	
FT		METAL	75	86	
FT		METAL	27	CALCIUM (VIA CARBONYL OXYGEN).	
FT		METAL	29	CALCIUM (VIA CARBONYL OXYGEN).	
FT		METAL	31	CALCIUM (VIA CARBONYL OXYGEN).	
FT		METAL	48	CALCIUM.	
FT		LIPID	7	N(6)-palmityl lysine.	
FT		LIPID	10	N(6)-palmityl lysine.	
FT		HELIX	2		
FT		HELIX	17		
FT		STRAND	23		
FT		STRAND	25		
FT		STRAND	28		
FT		STRAND	39		
FT		STRAND	52		
FT		STRAND	53		
FT		STRAND	59		
FT		STRAND	61		
FT		STRAND	66		

RA Hopkins R. F., Jordon H., Moore T., Max S. J., Wang J., Hsieh F., Hong L., DR PIR; S29495; S29495.
 RA Diatchenko L., Mansina K., Farmer M. A., Rubin G. M., Casavant T. L., Scheetz T. E., DR HSSP; P14555; 1POD.
 RA Stapleton M., Soares M. B., Bonaldo M. F., Brownstein M. J., Udin T. B., Prange C., DR MGDB; MGI:1046412; Pla2g2a.
 RA Brownstein M. J., Udin T. B., Tohnyiuki S., Carninci P., Peters G. D., Abramson R. D., DR InterPro; IPR001211; PhospholipaseA2.
 RA Raha S. S., Loqueline N. A., Mulany S. J., Malek J. A., Gunaratne P. H., Richards S. A., McEwan P. J., McErterman K. J., Worley K. C., Hale S., Garcia A. M., Gay L. J., Hulyk S. W., DR PFam; PF00068; phospholipaseA2.
 RA Villalon D. K., Muzny D. J., Sodergren E. J., Lu X., Gibbs R. A., Fahey J., Helton E., Keittman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A. C., Shevchenko Y., Bouffard G. G., Blakesley R. W., Tochman J. W., Green B. D., Dickson M. C., Rodriguez A. C., Grimwood J., Schmutz J., Myers R. M., Butterfield Y. S. N., Krywinski M. I., Skalska U., Smailus D. E., Scherck A., Schein J. E., Jones S. J. M., Marras M. A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", DR PROSITE; PS00018; PA2_HIS; 1.
 RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [5] RP SEQUENCE OF 22-146 FROM N.A. DR PROSITE; PS00019; PA2 ASP; 1.
 RC STRAIN-B1B/C; TISSUE=Small intestine; DR Hydrolase; Lipid degradation; Calcium Membrane; Polymorphism.
 RX MEDLINE=04029355; PubMed=8267767;
 RA Mulherkar R., Rao R. S., Wagle A. J., "Enhancing factor, a Paneth cell specific protein from mouse small intestines: predicted amino acid sequence from RT-PCR amplified cDNA and its expression"; DR SIGNAL; 21
 RL Biophys. Res. Commun. 195:1254-1263 (1993).
 RN [6] RP PRELIMINARY SEQUENCE OF 22-41.
 RC TISSUE=Small intestine; DR Query Match 42.8%; Score 350; DB 1; Length 146;
 RX MEDLINE=94071967; PubMed=8250944; DR Best Local Similarity 53.1%; Pred. No. 4e-30;
 RA Mulherkar R., Rao R., Wagle A. S., Patki V., Deo M. G.; DR Matches 9; Mismatches 49; Indels 2; Gaps 2;
 RL Biophys. Res. Commun. 197:351-352 (1993). DR Sequence 146 AA; 16145 MN; AB904F6B3B1B45C7 CRC64;
 RN [7] DR
 RP PRELIMINARY SEQUENCE OF 22-41.
 RC TISSUE=Small intestine; DR
 RX MEDLINE=93146172; PubMed=84253615; DR
 RA Mulherkar R., Rao R., Rao L., Patki V., Chauhan V. S., Deo M. G.; DR
 RT "Enhancing factor protein from mouse small intestines belongs to the phospholipase A2 family"; DR
 RT "FUNCTION: May play a role in cell proliferation, by increasing the binding of EGF to the cells and thereby modulating its action. In doing so, this isozyme binds to a membrane-associated receptor distinct from the EGFR receptor and which could be a heparan-sulfate proteoglycan located on the cell membrane." DR
 RL FEBS Lett. 317:263-266 (1993). DR
 CC -!- TISSUE SPECIFICITY: Mainly in the Paneth cells adjacent to the stem population in the small intestines. Also expressed in regenerating liver and hyperplastic esophageal epithelium. DR
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acyl-2-glycerophosphocholine + a fatty acid anion. DR
 CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity). DR
 CC -!- SUBCELLULAR LOCATION: Membrane-associated. DR
 CC -!- TISSUE SPECIFICITY: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides. DR
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-CC
 CC -!- POLYMORPHISM: In strains 129/SV, B10.RII and C57BL/6, a polymorphism causes a frameshift and premature truncation of the protein, rendering it inactive. Strains BALB/C, C3H/He, DBA/1, DBA/2, NBL and NZB/NBL contain the normal protein while strain CD-1 is heterozygous for the mutation. DR
 CC -!- SIMILARITY: Belongs to the Phospholipase A2 family. DR
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 CC EMBL; X7266; CAAS5325.1; DR
 CC EMBL; U33358; AAC5252.1; DR
 CC EMBL; U20244; AAB0315.1; ALT_INIT. DR
 CC EMBL; BC045156; AAH45156.1; DR
 CC PIR; I48342; I48342.

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OM protein - protein search, using sw model

Run on: July 3, 2004, 05:13:08 ; Search time 30.0075 Seconds

(without alignments)
 1493.077 Million cell updates/sec

Title: US-10-088-092a-30

Perfect score: 817

Sequence: 1 M^KS^RP^HV^LV^FL^CL^IV^AL^VT^GN YN^RK^YA^HY^PN^KL^CT^GP^TP^C 142

Scoring table: BLOSUM62

Gap⁰ 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTRMBL 25:*

* * *

1: sp_archea;*

2: sp_bacteria;*

3: sp_fungi;*

4: sp_invertebrate;*

5: sp_invertebrate;*

6: sp_mammal;*

7: sp_mhc;*

8: sp_organelle;*

9: sp_phage;*

10: sp_plant;*

11: sp_rabbit;*

12: sp_virus;*

13: sp_vertebrate;*

14: sp_unclassified;*

15: sp_rvirus;*

16: sp_bacteriophage;*

17: sp_archeap;*

ALIGNMENTS

RESULT 1

ID	Q91Y34	PRELIMINARY	PRT;	146 AA.
AC	Q91Y34			
DT	01-DEC-2001	(TRIMBLrel: 19, Created)		
DT	01-DEC-2001	(TRIMBLrel: 19, Last sequence update)		
DT	01-Oct-2003	(TRIMBLrel: 25, Last annotation update)		
DE		Platelet phospholipase A2 precursor (Fragment).		
OS		Rattus norvegicus (Rat).		
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX		NCBI_TaxID10116;		
RN	[1]	SEQUENCE FROM N.A.		

RC STRAIN_Wistar; TISSUE=Blood;
 RA Liu T.T., Liang N.S., Meng Z.Q., Xie Y.A., Kuang Z.P., Li Y.;
 "Cloning and sequence determination of rat platelet phospholipase A2 from whole blood."

RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF365163; AAK20611; .

DR GO; GO:0005059; F:calcium ion binding; IBA.

DR GO; GO:0004623; F:phospholipase A2 activity; IBA.

DR InterPro; IPR01211; Phospholipase1A.

DR Pfam; PF00068; Phoslip_1.

DR PRINTS; PHPLIPSEA2.

DR PRODOM; PD00033; PhospholipaseA2; 1.

DR SMART; SM00085; PA2C; 1.

DR PROSITE; PS00119; PA2-ASP; 1.

DR PROSITE; PS00118; PA2-HIS; 1.

DR SIGNAL; .

FT SIGNAL; .

FT CHAIN; .

FT NON_TPR; 146 AA; 16306 MW;

SQ SEQUENCE; 146 AA; 16306 MW;

Query Match 44.2%; Score 361.5; DB 11; Length 146;

Best Local Similarity 47.9%; Pred No. 2.4e-33;

Matches 69; Conservative 18; Mismatches 50; Indels 7; Gaps 3;

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	361.5	44.2	146	11	Q91Y34		Q91Y34 rattus norvegicus
2	342.5	41.9	138	13	Q7TLD5		Q7TLD5 rattus beru
3	339.5	41.6	138	13	Q80533		Q80533 trimeresurus
4	337.5	41.3	138	13	Q8AXX1		Q8AXX1 bothrops ja
5	337.5	41.3	138	13	Q80542		Q80542 trimeresurus
6	330.5	40.5	138	13	Q7ZTA8		Q7ZTA8 crotaalus vi
7	329.5	40.3	138	13	Q7ZTA6		Q7ZTA6 crotaalus vi
8	328.5	40.2	138	13	Q7TID1		Q7TID1 viper beru
9	327.5	40.1	138	13	Q7TID4		Q7TID4 viper aspis
10	327.5	40.1	138	13	Q7TID3		Q7TID3 viper aspis
11	327.5	40.1	138	13	Q7TID2		Q7TID2 viper aspis
12	322.5	39.5	138	13	Q800C1		Q800C1 crotaalus vi
13	321.5	39.4	138	13	Q800C2		Q800C2 crotaalus vi
14	321.5	39.4	138	13	Q7ZTA7		Q7ZTA7 crotaalus vi
15	317.5	38.9	138	13	Q800C4		Q800C4 crotaalus vi
16	317.5	38.9	187	4	Q8N435		Q8N435 homo sapien

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

QY	6	VLYPLCLLVAL --- - VTNGLNLYCGYMIEKMTGKSA - LOXNDYGGYCYGIGGSHHWVFDQTD
Dbb	3	VLLILAVIMAFGSSLLEFGQNPPTKGRADVSFGYGCVGQRSKSKDADT
QY	60	WCCHAHDCCYGRILKEPKLGFPSVSERGIFCA - GRITCQRLTCEDCDKRALCFFR
Db	63	WCCVTHDCYCNRLERGGTKFLTYKFSYRGGRISCSNTQDSCKRQLCQCDKAEECFAR
QY	119	NLGTYRNKRYAHYPNKLCTGPTPFC
Db	123	NKCKSYSLKQFYPRKFCKGKTPSC
QY	142	
Db	146	

RESULT 2					
	Q77115	PRELIMINARY;	PRT;	138 AA.	
Q77115	Q77115;				
Q77115;	01-OCT-2003	{TREMBrel.	25,	Created	
Q77115;	01-OCT-2003	{TREMBrel.	25,	Last sequence update	
Q77115;	01-OCT-2003	{TREMBrel.	25,	Last annotation update	
PLA2B.					
DB					
Phospholipase A2.					
GN					
PLA2B.					
OS	Vipera berus berus	(Common viper).			
OS	Bufo bufo				
OC	Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;				
OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;				
OC	Viperidae; Viperinae; Vipera.				
NCBI_TaxID	31156;				
RN	111				
RN	SEQUENCE N.A.				
RP	SEQUENCE N.A.				
RP	MEDLINE=2270820; PubMed=12823540;				
RA	Guillemin I.; Bouchier C.; Garrigues T.; Wisner A.; Choumet V.;				
RA	"Sequences and structural organization of phospholipase A2 genes from				
RT	Vipera aspis aspis. V. aspis zimnikeri and Vipera berus berus venom.				
RT	Identification of the origin of a new viper population based on				
RT	ammonodytin II heterogeneity."				
RT	*Eur J. Biochem. 270:2497-2506 (2003).				
RL					

RESULT 3		PRELIMINARY;		PRT;	138 AA.
QY	Q805A3	ID	Q805A3;		
Db	132	AC	Q805A3;		
		DT	01-JUN-2003	(TREMBLrel.	24, Created
		DT	01-JUN-2003	(TREMBLrel.	24, Last sequence update)
		DT	01-OCT-2003	(TREMBLrel.	25, Last annotation update)
		DE	Phospholipase A2.		
		GN	PLA_N.		
		OS	Trimeresurus flavoviridis (Habu).		
		OS	Trimeresurus; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei;		
		CC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubridae;		
		CC	Viperidae; Crotalinae; Trimeresurus.		
		OC	NCBI_TaxID=88087;		
		OX	[1]		
		RN	SEQUENCE FROM N.A.		
		RP			

Chihiwa T., Hama S., Tsubouchi S., Ogawa T., Deshimaru M., Oda-Ueda N., Hattori S., Kihara H., Tsunazawa S., Ohno M.; "Interisland mutation of a novel phospholipase A2 from Trimeresurus flavoviridis venom and evolution of crotaline group II phospholipases A2.", Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB102228; BAC5892.1; "
DR GO; GO:0005519; F:calcium ion binding; IEA.
DR GO; GO:0004223; F:phospholipase A2 activity; IEA.
DR GO; GO:0016042; P:Lipid catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00088; Phoslip; 1.
DR PRINTS; PR00389; PHMPHIPASEA2.
DR PRODOM; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2C; 1.
DR PROSITE; PS00119; PA2 ASP; 1.
DR PROSITE; PS00118; PA2 HIS; 1.
DR SEQUENCE; 138 AA; 15817 MW; A2FB5SA23897ECC5 CRC64;
Query Match 41.6%; Score 339.5; DB 13; Length 138;
Best Local Similarity 47.4%; Pred. No. 7.4e-11;
Matches 65; Conservative 16; Mismatches 53; Indels 3; Gaps 1
QY 7 LVFCLLVALVGNLQVGVMIERMTGKASALO-YNDYCYCIGIGSSHW PYDQDTDMCCHI
Db 4 LWIMAVLLVGVGNLQFNKMKMVKPCKNGFPYTFVTCRDLCEKQICEDRAAVFGQNLRVY
QY 66 DCCYGRLEKLGCPEPKLEYLFVSVSERGFCAAGRTTCORLTCDKREALAFCPRNLGTYY
Db 64 DCCYERKL--TDCCSPKSDDIYSWMSWKTGVICGBGTECEKQICEDRAAVFGQNLRVY
QY 126 KYAHYNPKLCTGTPPPC 142
Db 122 KTMFYPPDLCDDPTEKC 138
RESULT 4
Q8AXY1 PRELIMINARY; PRT; 138 AA.
ID Q8AXY1; AC Q8AXY1; DT 01-MAR-2003 (TREMBLrel. 23; Created)
AC Q8AXY1; DT 01-MAR-2003 (TREMBLrel. 23; Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25; Last annotation update)
DE Hypotensin-like phospholipase A2.
OS Bothrops jararacussu [Jararacussu].
OC Buthidae.
OC Metastoma; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothriops.
OC NCB_—TaxID=8726;
RN [1] N
RP SEQUENCE FROM N.A.
RC TISSUE=Venom Gland;
RC MEDLINE=22167491; PubMed=12167491;
RA Andriao-Escarso S.H., Soares A.M., Fontes M.R., Fuly A.L., Pranca S.C.;
RA Correa F.M., Rosa J.C., Green L.J., Giglio J.R.;
RA "Functional and Structural Analysis of an acidic platelet A2 from Bothrops jararacussu Snake Venom";
RA aggregation inhibitor and hypotensive phospholipase A(2) from Bothrops jararacussu snake venom."
RL Biochem Pharmacol. 64:723-732 (2002).
[2]
RN SEQUENCE FROM N.A.
RC TISSUE=Venom Gland;
RC Robert P.G., Kashima S., Soares A.M., Astolfi-Filho S., Giglio J.R.
RA "Structural and Functional characterization of an acidic platelet A2 from Bothrops jararacussu Snake Venom";
RA Submitted (AUT-2002) to the EMBL/GenBank/DDBJ databases.
RL EMBL; AY145838; AN37410.1; "
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR GO; GO:0016042; P:Lipid catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
Pfam; PF00088; Phoslip; 1.
DR

DR	PRINTS; PR00389; PHOSPHOLIPASEA2.	Db	122 KTMFYPPDFLCTDETEKC 138
DR	SMART; SM00085; PA2c; 1.		
DR	PROSITE; PS00119; PA2 ASP; 1.		
DR	PROSITE; PS00118; PA2 HIS; 1.		
SQ	SEQUENCE 138 AA; 15456 MW; 513647907BFDQF4E CRC64;	RESULT 6	
	Query Match Score 337.5; DB 13; Length 138;	ID Q7ZTA8	PRELIMINARY;
	Best Local Similarity 45.3%; Pred. No. 1.3e-30;	AC Q7ZTA8;	PRT; 138 AA.
	Matches 62; Conservative 19; Mismatches 53; Indels 3; Gaps 2;	DT 01-JUN-2003 (TREMBLrel. 24, Created)	
	QY 7 LVFLCLVALVTGNLQFGMILRKIGRS-ALQNDYGGCGTGSHWVTDQDWCCAH 65	DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)	
Db	4 IWMIAVLGVVEGSLWQRGRMINVYMGESCVLQVLSYGCYGLGQGQTDAEDRCCFTVH 63	DE Acidic phospholipase A2.	
Qy	66 DCCYGRKVLPEKLTFLFSVSRGRIIFAGRTRICORLTCECDRAALCFRNLTYNR 125	OS Crotalus viridis (Prairie rattlesnake).	
Db	64 DCCYGRKV--TGCDPKIDSTYTSKNGDVGDDPCKKQICECDRATCFRDNKD7D1 121	OC Lepidosaura; Chordata; Craniata; Vertebrata; Buteleostomi; Colubroidea; Viperidae; Crotalinae; Crotalus.	
Qy	126 KYAHYPNKLCTGTPPC 142	OC Viperidae; Crotalinae; Crotalus.	
Db	122 KYWFYGAHKQERKSEPC 138	OX NCBI_TaxID=8742;	
	SEQUENCE FROM N.A.	RN [1];	
	STRAIN/AGE:	RX	
	MEDLINE=22510024; PubMed=12623078;	GO GO-0000509 F:calcium ion binding; IEA.	
	GO GO-00016042; P:lipid catabolism; IEA.	DR DR	
	INTERPRO: IPR01211; PhospholipaseA2.	DR DR	
	PFAM: PF00068; PhosphiP_1;	DR DR	
	PRINTS: PR00389; PHOSPHOLIPASEA2.	DR DR	
	PRODOM: PD000303; PhospholipaseA2; 1.	DR DR	
	SMART: SM00085; PA2c; 1.	DR DR	
	PROSITE; PS00119; PA2 ASP; 1.	DR DR	
	PROSITE; PS00118; PA2 HIS; 1.	DR DR	
	SEQUENCE 138 AA; 15414 MW; 4435EA1FE6A39D0 CRC64;	SQ	
	Query Match Score 330.5; DB 13; Length 138;	Query Match Score 330.5;	
	Best Local Similarity 45.3%; Pred. No. 8e-30; Mismatches 54; Indels 3; Gaps 2;	Best Local Similarity 45.3%; Pred. No. 8e-30; Mismatches 54; Indels 3; Gaps 2;	
	Matches 62; Conservative 18; Mismatches	Matches 62; Conservative 18; Mismatches	
Q805A2	PRELIMINARY;	QY 7 LVFLCLVALVTGNLQFGMIEKMTGKSA-LQXNDYGCYCIGGSHWVTDQDWCCAH 65	
ID Q805A2	PRT; 138 AA.	RT InterPro: IPR01211; PhospholipaseA2.	
AC Q805A2;	DT 01-JUN-2003 (TREMBLrel. 24, Created)	RT PFAM: PF00068; PhosphiP_1;	
DT 01-OCT-2003 (TREMBLrel. 24, Last sequence update)	DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)	RT PRINTS: PR00389; PHOSPHOLIPASEA2.	
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)	DR PRODOM: PD000303; PhospholipaseA2; 1.	DR SMART: SM00085; PA2c; 1.	
DE PLA-N(O).	DR PROSITE; PS00119; PA2 ASP; 1.	DR PROSITE; PS00118; PA2 HIS; 1.	
GN PLA2.	DR PROSITE; PS00118; PA2 HIS; 1.	DR PROSITE; PS00118; PA2 HIS; 1.	
OS Trimeresurus flavoviridis (Habu).	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	
OC Eutherocotylidae; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Colubroidea; Viperidae; Crotalinae; Trimeresurus.	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	
NCB_TaxID=88087;	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	
RN [1];	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	
SEQUENCE FROM N.A.	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	
RA Chihiwa T., Hamai S., Tsubouchi S., Ogawa T., Deshimaru M., Oda-Ueda N., Hattori S., Kihara H., Tsunashima S., Ohno M.,	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	
RT "Interstrand mutation of a novel phospholipase A2 from Trimeresurus flavoviridis venom and evolution of crotalinae group II phospholipase A2".	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	
EMBL: ABI02729; BAC56893.1;	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	
DR GO: GO:0005505; P:calcium ion binding; IEA.	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	
DR GO: GO:0004623; P:lipid catabolism; IEA.	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	
DR GO: GO:0016042; P:lipid catabolism; IEA.	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	
DR InterPro: IPR01211; PhospholipaseA2.	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	
DR Pfam: PF00068; PhosphiP_1.	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	
DR PRODOM: PD000303; PhospholipaseA2; 1.	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	
DR SMART; SM00085; PA2c; 1.	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	
DR PROSITE; PS00119; PA2 ASP; 1.	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	
DR PROSITE; PS00118; PA2 HIS; 1.	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	
SQ SEQUENCE 138 AA; 15503 MW; A2F103123897ECC5 CRC64;	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	DR PRINTS: PR00389; PHOSPHOLIPASEA2.	
RESULT 7	ID Q7ZTA6	PRELIMINARY;	PRT; 138 AA.
	AC Q7ZTA6;		
	DT 01-JUN-2003 (TREMBLrel. 24, Created)		
	DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)		
	DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
	DE Acidic phospholipase A2.		
	OS Crotalus viridis (Prairie rattlesnake).		
	OC Lepidosaura; Chordata; Craniata; Vertebrata; Buteleostomi; Colubroidea; Viperidae; Crotalinae; Crotalus.		
	NCB_TaxID=8742;		
	SEQUENCE FROM N.A.	RN [1];	
	STRAIN/AGE:	RX	
	MEDLINE=22510024; PubMed=12623078;	GO GO-0000509 F:calcium ion binding; IEA.	
	GO GO-00016042; P:lipid catabolism; IEA.	DR DR	
	INTERPRO: IPR01211; PhospholipaseA2.	DR DR	
	PFAM: PF00068; PhosphiP_1;	DR DR	
	PRINTS: PR00389; PHOSPHOLIPASEA2.	DR DR	
	PRODOM: PD000303; PhospholipaseA2; 1.	DR DR	
	SMART: SM00085; PA2c; 1.	DR DR	
	PROSITE: PS00119; PA2 ASP; 1.	DR DR	
	PROSITE: PS00118; PA2 HIS; 1.	DR DR	
	SEQUENCE 138 AA; 15503 MW; A2F103123897ECC5 CRC64;	DR DR	
	Query Match Score 337.5; DB 13; Length 138;	DR DR	
	Best Local Similarity 47.4%; Pred. No. 1.3e-30;	DR DR	
	Matches 65; Conservative 15; Mismatches 54; Indels 3; Gaps 2;	DR DR	
QY 7 LVFLCLVALVTGNLQFGMIEKMTGKSA-LQXNDYGCYCIGGSHWVTDQDWCCAH 65	DR DR		
Db 4 IWMIAVLGVVEGSLWQRGRMINVYMGESCVLQVLSYGCYGLGQGQTDAEDRCCFTVH 63	DR DR		
QY 66 DCCYGRKVLPEKLTFLFSVSRGRIIFAGRTRICORLTCECDRAALCFRNLTYNR 125	DR DR		
Db 64 DCCYGRKV--TGCDPKIDSTYTSKNGDVGDDPCKKQICECDRATCFRDNKD7D1 121	DR DR		
Qy 126 KYAHYPNKLCTGTPPC 142	DR DR		

"Geographic variations, cloning, and functional analyses of the venom

"Geographic variations, cloning, and Functional analyses of the venom

RESULT 9

Q7T1D4	PRELIMINARY;	PRT;	138 AA.
ID Q7T1D4			
AC Q7T1D4			
SEQNCE FROM N.A.			
RN [1]			
RP SEQUENCE FROM N.A.; PubMed=12823540;			
RX MEDLINE=22707820; PubMed=12823540;			
RA Guillemin I., Bouchier C., Garrigues T., Wisner A., Choumet V.;			
RT "Sequences and structural organization of phospholipase A2 genes from Vipera aspis aspis, V. aspis zinnikeri and Vipera berus berus venom."			
RT Identification of the origin of a new viper population based on ammonitin II heterogeneity".			
RT Eur. J. Biochem. 270:697-2706 (2003).			
RL EMBL: AY159808; AAN59987.1; -.			
SQ SEQUENCE 138 AA; 15414 MW; C4C985F113EC5DB6 CRC64;			

Query Match 40.3%; Score 329.5; DB 13; Length 138;

Best Local Similarity 45.3%; Pred. No. 1e-29; Mismatches 54; Indels 3; Gaps 2;

Matches 62; Conservative 18; Mismatches 54;

Qy 7 LVFLCLLVAVTGNLVQFGWMIEPTGRSA-LQIINDIGYCGIGGSWHDQDWCCAH 65

Db 4 IWLAVLLGVEGNLVQFELLIMVAKRSGLLS TSAYGYCGWGGYGRPODAIDRCCEFH 63

Qy 66 DCCYGRLEKLGCPKLEKTFPSVSRGIFPAGRTICQRLTCEDCKRALCFRRNLGTYNR 125

Db 64 DCCYGRKV-.TDCNPKTASITYSEENGETIVGGDDPCKQVCECDRVAAICFGEMNTDK 121

Qy 126 KYAHYPNKLCTGPTPPC 142

Db 122 KYIQFPKRNQEKPEPC 138

RESULT 8

Q7T1D1	PRELIMINARY;	PRT;	138 AA.
ID Q7T1D1			
AC Q7T1D1			
SEQNCE FROM N.A.			
RN [1]			
RP SEQUENCE FROM N.A.; PubMed=12823540;			
RX MEDLINE=22707820; PubMed=12823540;			
RA Guillemin I., Bouchier C., Garrigues T., Wiener A., Choumet V.;			
RT "Sequences and structural organization of phospholipase A2 genes from Vipera aspis aspis, V. aspis zinnikeri and Vipera berus berus venom."			
RT Identification of the origin of a new viper population based on ammonitin II heterogeneity".			
RT Eur. J. Biochem. 270:2697-2706 (2003).			
RL EMBL: AY159811; AAN59990.1; -.			
SQ SEQUENCE 138 AA; 15414 MW; 7E8D1EFT070880403 CRC64;			

Query Match 40.2%; Score 328.5; DB 13; Length 138;

Best Local Similarity 46.7%; Pred. No. 1.4e-29; Mismatches 52; Indels 5; Gaps 3;

Matches 64; Conservative 16; Mismatches 52;

Qy 7 LVFLCLLVAVTGNLVQFGWMIEPTGR-.SALQIINDIGYCGIGGSWHDQDWCCAH 65

Db 6 IVAVLIGA--EGNLSQFGDNINKTKTGIFGIMSYIYGCGWGGKGRLEIDATRCCEFH 63

Qy 66 DCCYGRLEKLGCPKLEKTFPSVSRGIFPAGRTICQRLTCEDCKRALCFRRNLGTYNR 125

Db 64 DCCYGRKV-.GDPKPLSTSYSSFENGDIVGGDDPCLRAYCEDRVAAICFGEMNTDK 121

Qy 126 KYAHYPNKLCTGPTPPC 142

Db 122 KYMLYSFLDCKBESEOC 138

RESULT 10

Q7T1D3	PRELIMINARY;	PRT;	138 AA.
ID Q7T1D3			
AC Q7T1D3			
SEQNCE FROM N.A.			
RN [1]			
RP SEQUENCE FROM N.A.; PubMed=12823540;			
RX MEDLINE=22707820; PubMed=12823540;			
RA Guillemin I., Bouchier C., Garrigues T., Wisner A., Choumet V.;			
RT "Sequences and structural organization of phospholipase A2 genes from Vipera aspis aspis, V. aspis zinnikeri and Vipera berus berus venom."			
RT Identification of the origin of a new viper population based on ammonitin II heterogeneity".			
RT Eur. J. Biochem. 270:2697-2706 (2003).			
RL EMBL: AY159808; AAN59987.1; -.			
SQ SEQUENCE 138 AA; 15414 MW; C4C985F113EC5DB6 CRC64;			

Query Match 40.1%; Score 327.5; DB 13; Length 138;

Best Local Similarity 46.7%; Pred. No. 1.8e-29;

PRINTS; PRO00389; PHIPHILIPASEA2; 1.
DR Prodom; PD000303; PhospholipaseA2; 1.
DR SMART; SNO085; PACC; 1.
DR PROSITE; PS00119; PA2 ASP; 1.
DR PROSITE; PS00118; PA2 HIS; 1;
SQ SEQUENCE 138 AA; 15556 MW; 09134B8AB3EE3723 CRC64;

Query Match Score 321.5; DB 13; Length 138;
Best Local Similarity 44.5%; Pred. No. 8.6e-29;
Matches 61; Conservative 17; Mismatches 56; Indels 3; Gaps 2;

Qy 7 LVFLCLVALTGNLIVQFGMIEIWTGKSA-LQYNDYCGGSHWPVDOTDWCCAH 65
Db 4 LWIVAVLLVEGSIVQFEMIIVKVARSGFLWGAAYCYGRGGQRQDPAIDTRCCFVH 63

Qy 66 DCCYGRLEKKGCEPKLEYKIVFSERGICIAAGRTTCQBLTCECDKRALCFRNLTGYNR 125
Db 64 DCCYGRK-ATDCNPKTVSIVTYSVRGETICEDDPCKQVCBDRVAACFRDNIPSYNN 121

Qy 126 KYAHYPNKLCTGTPPPC 142
Db 122 NYKEPPAENCRGDPEPPC 138

RESULT 14
Q7ZTA7 PRELIMINARY; PRT; 138 AA.
ID Q7ZTA7
AC DT 01-JUN-2003 (TREMBREL. 24, Created)
DT 01-JUN-2003 (TREMBREL. 24, Last sequence update)
DT 01-OCT-2003 (TREMBREL. 25, Last annotation update)
DE "Acidic phospholipase A2."
OS Crotalus viridis (Prairie rattlesnake).
OC Lepidosauria; Squamata; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Viperidae; Crotalinae; Crotalidae; Colubroidea;
OX NCBI_TaxID=8742;

Query Match Score 321.5; DB 13; Length 138;
Best Local Similarity 43.8%; Pred. No. 8.6e-29;
Matches 60; Conservative 20; Mismatches 54; Indels 3; Gaps 2;

Qy 7 LVFLCLVALTGNLIVQFGMIEIWTGKSA-LQYNDYCGGSHWPVDOTDWCCAH 65
Db 4 LWIVAVLLVEGSIVQFEMIIVKVARSGFLWGAAYCYGRGGQRQDPAIDTRCCFVH 63

Qy 66 DCCYGRLEKKGCEPKLEYKIVFSERGICIAAGRTTCQBLTCECDKRALCFRNLTGYNR 125
Db 64 DCCYGRK-ATDCNPKTVSIVTYSVGETYGGDDPCKQVCBDRVAACFRDNIPSYNN 121

Query Match Score 321.5; DB 13; Length 138;
Best Local Similarity 43.8%; Pred. No. 8.6e-29;
Matches 60; Conservative 20; Mismatches 54; Indels 3; Gaps 2;

Qy 7 LVFLCLVALTGNLIVQFGMIEIWTGKSA-LQYNDYCGGSHWPVDOTDWCCAH 65
Db 4 LWIVAVLLVEGSIVQFEMIIVKVARSGFLWGAAYCYGRGGQRQDPAIDTRCCFVH 63

Qy 66 DCCYGRLEKKGCEPKLEYKIVFSERGICIAAGRTTCQBLTCECDKRALCFRNLTGYNR 125
Db 64 DCCYGRK-ATDCNPKTVSIVTYSVGETYGGDDPCKQVCBDRVAACFRDNIPSYNN 121

Qy 126 KYAHYPNKLCTGTPPPC 142
Db 122 KYWLPFLPKNRGDPPEPC 138

SEARCH COMPLETED: July 3, 2004, 05:17:44
Job time : 33.0075 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2004 Compugen Ltd.
 OM protein - protein search, using sw model
 Run on: July 3, 2004, 05:12:17 ; Search time 40.1887 Seconds
 (without alignments)
 998.335 Million cell updates/sec
 Title: US-10-088-092A-30
 Perfect score: 817
 Sequence: 1 MKSPHVLVFLCLIVLVTCN.....YNEKVAIYPNKLUCTGPTPPC 142
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Searched: 1586107 seqs, 282547505 residues
 Total number of hits satisfying chosen parameters: 1586107

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : A_GenSeq_29Jan04:*

database :		%	Query	Score	Match	Length	DB	ID
	result No.		No.					
1: _Geneset_29Jan04: *	1	817	100.0	142	4	AAB81		
1: _Geneset_1980s: *	2	817	100.0	154	6	ABR44		
2: _Geneset_1990s: *	3	817	100.0	154	6	ABU63		
3: _Geneset_2000s: *	4	709	86.8	142	3	AAB112		
4: _Geneset_20015: *	5	709	86.8	142	4	AAB81		
5: _Geneset_2004s: *	6	370	45.3	164	3	AAB81		
6: _Geneset_2003bs: *	7	368.5	45.1	144	1	AAZ93		
7: _Geneset_2003bs: *	8	368.5	45.1	144	2	AAZ93		
8: _Geneset_2004s: *	9	368.5	45.1	144	2	AAZ93		
	10	368.5	45.1	144	2	AAZ93		
	11	368.5	45.1	144	6	ABR44		
	12	368.5	45.1	144	6	ABR44		
	13	368.5	45.1	144	6	ABU63		
	14	368.5	45.1	144	7	ADB75		
	15	368.5	45.1	144	7	ADB63		
	16	363.5	44.5	124	6	ADA61		
	17	360.5	44.1	124	2	AAR10		
	18	360.5	44.1	124	2	AHW73		
	19	360.5	44.1	124	6	ADA61		
	20	360.5	44.1	124	6	ADA61		
	21	360.5	44.1	124	6	ABR83		
	22	359.5	44.0	146	7	ADBE3		
	23	357.5	43.8	124	6	ADA61		
	24	351	43.0	145	2	AAR63		
	25	350	43.0	145	2	AAR63		

					Abb08154 Murine PL
26	350	42.8	146	5	Abb08154 Murine PL
27	350	42.8	146	6	Abb09808 Mouse pho
28	348	42.6	125	2	Aar63160 Rat PLA2
29	331.5	40.6	122	3	Aay88892 Ratskistrod
30	329	40.3	144	3	Aab12336 Mouse sec
31	329	40.3	144	3	Aab11944 Mouse sec
32	317.5	38.9	138	2	Aar61046 HPLA2-10.
33	317.5	38.9	138	6	Abr44237 Human sec
34	317.5	38.9	138	6	Aae31571 Human pho
35	317.5	38.9	138	6	Abu63126 Human gro
36	317.5	38.9	138	7	Add47911 Human Pro
37	317.5	38.9	138	7	Add47915 Human Pro
38	317.5	38.9	138	7	Add47919 Human Pro
39	314.5	38.5	132	2	Aaw58476 Human syn
40	314.5	38.5	137	2	Aar63045 PLA2-10.
41	314.5	38.5	137	7	Add47917 Rat Prote
42	314.5	38.5	137	7	Add47909 Rat Prote
43	314.5	38.5	137	7	Add47913 Rat Prote
44	310.5	38.0	145	4	Aau05096 Novel hum
45	310.5	38.0	145	6	Abr44234 Human sec

ALIGNMENTS

RESULT 1

AAB81022 standard; protein; 142 AA.
12-JUN-2001 (first entry)
Human Phospholipase A2 (PLA2) amino acid sequence.
Phospholipase A2; PLA2; antibacterial; immunosuppressive; pulmonary; antiinflammatory; tranquiliser; antiasthmatic; antiallergic; trauma; antirheumatic; antiarthritic; septic shock; pancreatic; human; adult respiratory distress syndrome; ARDS; bronchial asthma; allergic rhinitis; rheumatoid arthritis.

result No.	Score	Query	Match	Length	DB	ID	Description
1	817	100.0	142	4	AAB81022		Aab81022 Human P
2	817	100.0	154	6	AB44235		Abr44235 Human S
3	817	100.0	154	6	ABU65125		Abu65125 Human G
4	709	86.8	142	3	AAB81810		Aab81810 Mouse S
5	709	86.8	142	4	AAB81021		Aab81021 Murine L
6	370	45.3	164	3	AAB86432		Aab86432 Human P
7	368.5	45.1	144	1	AAP93112		Aap93112 Human I
8	368.5	45.1	144	1	AAP93363		Aap93363 Human S
9	368.5	45.1	144	2	AAR21416		Aar21416 PLA2, 1
10	368.5	45.1	144	2	AAR65055		Aar65055 Human P
11	368.5	45.1	144	6	ABP41233		Abp41233 Human S
12	368.5	45.1	144	6	ABP6807		Abp6807 Human P
13	368.5	45.1	144	6	ABU53123		Abu53123 Human G
14	368.5	45.1	144	7	ADB5501		Adb5501 Prostate
15	368.5	45.1	144	7	ADD36560		Adc36560 Human P
16	363.5	44.5	124	6	AAR1984		Aar1984 Human I
17	360.5	44.1	124	6	AAR0126		Aar0126 Membrane
18	360.5	44.1	124	2	AAW73562		Aaw73562 Human G
19	360.5	44.1	124	6	ADE1982		Adc1982 Human G
20	360.5	44.1	124	6	AD61978		Ad61978 Human G
21	360.5	44.1	124	6	ABR82569		Abr82569 Human G
22	359.5	44.0	124	7	ADE33558		Adc33558 Rat Pro
23	357.5	43.8	124	6	AD61983		Ad61983 Human T
24	351.0	43.0	145	2	ABE30053		Abe30053 HPLA2-8
25	351.0	43.0	145	2	AAB63053		Aab63053 HPLA2-8

XX Human secretory phospholipase A2 and encoded gene, useful in diagnosis of
PT and screening drug candidates for treating associated diseases e.g.
PT septic shock, adult respiratory distress syndrome and rheumatoid
PT arthritis.

XX Claim 1; Page 46-47; 50pp; Japanese.

XX

and the gene encoding it. Inhibitors of phospholipase A2 have antibacterial; immunosuppressive; antiinflammatory; tranquiliser; vulnery; antiasthmatic; antiallergic; and antiarthritic activity. The PLA2 protein, gene and an anti-PLA2 antibody are useful in the diagnosis of PLA2 associated diseases e.g. septic shock, adult allergic rhinitis, respiratory distress syndrome, pancreatitis, trauma, bronchial asthma, allergic rhinitis and rheumatoid arthritis. The present sequence represents human PLA2.

Sequence 142 AA;

Query Match 100.0%; Score 817; DB 4; Length 142;
Best Local Similarity 100.0%; Pred. No. 1.5e-67;
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKSPHVLVFLCLLVALTGNLYQFGWMIEKMTGKSAQNYDGYCGYCGIGSHWVVDQTDW 60
Db 1 MKSPHVLVFLCLLVALTGNLYQFGWMIEKMTGKSAQNYDGYCGYCGIGSHWVVDQTDW 60
Qy 61 CCHAHDCCYGRLEKLGEPKLERYLFLVSERGIFCAGRITCQRLTCECDRAALCFRNL 120
Db 61 CCHAHDCCYGRLEKLGEPKLERYLFLVSERGIFCAGRITCQRLTCECDRAALCFRNL 120
Qy 121 GTYNRKTAHYPNKLCTGTPPPC 142
Db 121 GTYNRKTAHYPNKLCTGTPPPC 142

RESULT 2
ABR44235
ID ABR44235 standard; protein; 154 AA.
XX AC ABR44235;

AC 18-AUG-2003 (first entry)

DE Human secreted group IIF phospholipase A2 (sPLA2) enzyme.

XX Group IIF secreted phospholipase A2; sPLA2; phosphatidylglycerol; human; phosphatidylcholine; antibacterial; virucide; cytostatic; vasoconstrictive; antiinflammatory; pulmonary; cytosolic; vasoconstrictive; enzyme.

XX Homo sapiens.

OS WO2003033689-A1.

XX PD 24-APR-2003.

XX PP 12-OCT-2001; 2001WO-1B002407.

XX PR 12-OCT-2001; 2001WO-1B002407.

(CNRS) CNRS CENT NAT RECH SCI.

XX PI Lazdunski M, Lambeau G, Valentin E;

XX DR 2003-103216/3.

XX PS Novel mammalian secreted group IIF secreted phospholipase A2, useful for preventing and treating bacterial and viral infections, and cancers.

XX Disclosure: Fig 1; 33pp; English.

XX CC The invention relates to a mammalian secreted group IIF secreted phospholipase A2 (sPLA2) (I), where the enzyme is Ca²⁺ dependent, maximally active at pH 7-8 and hydrolyses phosphatidylglycerol versus phosphatidylcholine with a 15-fold preference. A pharmaceutical composition comprising (I) is useful for treating or preventing viral and bacterial infections, and cancers. A pharmaceutical composition containing compounds capable of inhibiting catalytic activity of (I), biologically active compounds that bind sPLA2 receptors, or a compound that modulates cell proliferation, cell migration, cell contraction or

CC apoptosis is useful for treating disease states or disorders involving group IIF sPLA2, such as inflammatory disease, cancers, cardiac and brain ischaemia, acute lung injury, acute respiratory distress syndrome or Crohn's disease. Specific antibodies are useful for diagnosing new secreted mammalian group IIF sPLA2 or the homologues of the enzyme in other mammals. The encoding polynucleotides and vectors are useful for transforming animals and establishing a line of transgenic animals. Sequences ABR4232-238 represent various human secreted sPLA2 enzymes used in alignment studies with the GIIF sPLA2 enzyme.

SQ Sequence 154 AA;

Query Match 100.0%; Score 817; DB 6; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.6e-67;
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKSPHVLVFLCLLVALTGNLYQFGWMIEKMTGKSAQNYDGYCGYCGIGSHWVVDQTDW 60
Db 13 MKSPHVLVFLCLLVALTGNLYQFGWMIEKMTGKSAQNYDGYCGYCGIGSHWVVDQTDW 72
Qy 61 CCHAHDCCYGRLEKLGEPKLERYLFLVSERGIFCAGRITCQRLTCECDRAALCFRNL 120
Db 73 CCHAHDCCYGRLEKLGEPKLERYLFLVSERGIFCAGRITCQRLTCECDRAALCFRNL 132
Qy 121 GTYNRKTAHYPNKLCTGTPPPC 142
Db 133 GTYNRKTAHYPNKLCTGTPPPC 154

RESULT 3

ABU61125
ID ABU61125 standard; protein; 154 AA.

XX AC ABU61125;

XX DT 25-SEP-2003 (first entry)

DE Human group IIB secreted phospholipase A2.

XX Human; group IIE secreted phospholipase A2; virucide; antibacterial; cytosolic; antiinflammatory; vasoconstrictive; sPLA2; phosphatidylglycerol hydrolysis; phosphatidylcholine hydrolysis; viral infection; bacterial infection; cancer; inflammatory disease; cardiac ischaemia; brain ischaemia; acute lung injury; acute respiratory distress syndrome; Crohn's disease; enzyme. XX Homo sapiens.

XX OS WO2003073087-A1.

XX PN US2003073087-A1.

XX PD 17-APR-2003.

XX PF 11-OCT-2001; 2001US-00975456.

XX PR 11-OCT-2000; 2000US-0239491-P.

XX PA (LAZDUNSKI) LAZDUNSKI M.

PA (LAMBEAU) LAMBEAU G.

PA (VALENTIN) VALENTIN E.

XX PI Lazdunski M, Lambeau G, Valentin E;

XX DR WPI; 2003-1567302/53.

XX New mammalian secreted group IIF phospholipase A2 or nucleic acid, useful for treating or preventing viral or bacterial infections, or cancers, or screening inhibitors of the enzyme for treating e.g. inflammatory diseases or ischaemia. XX Disclosure: Fig 1; 16pp; English.

XX The invention describes a mammalian secreted group IIF phospholipase A2 (sPLA2), which is Ca²⁺-dependent, maximally active at pH of about 7-8,

CC and hydrolyses phosphatidylglycerol versus phosphatidylcholine with about
 CC a 15-fold preference. The mammalian secreted group IIE sPLA2 protein or
 CC nucleic acid, or a pharmaceutical composition useful for treating
 CC and/or preventing viral infections, bacterial infections, or cancers. The
 CC inhibitors of sPLA2 or a composition comprising sPLA2 inhibitors is
 CC useful for treating disease states or disorders involving group IIE
 CC sPLA2, e.g. inflammatory diseases, cancer, cardiac and brain ischaemia,
 CC acute lung injury, acute respiratory distress syndrome, or Crohn's
 CC disease. The enzyme is also useful for screening various chemical
 CC compounds for treating these diseases. This is the amino acid sequence of
 CC human group IIE phospholipase A2 used to determine a consensus sequence
 CC for human sPLA2s

XX Sequence 154 AA;
 XX

Query Match Score 817; DB 6; Length 154;
 Best Local Similarity 100.0%; Pred. No. 1.6e-67;
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
 AAB8101
 ID AAB8101 standard; protein; 142 AA.

QY 1 MKSPHVLVFLCLLYVALVGNLIVQFGVMIKEMTGKSAQLQNDYGCYCGIGGSHKRPVDQDW 60
 Db 13 MKSPHVLVFLCLLYVALVGNLIVQFGVMIKEMTGKSAQLQNDYGCYCGIGGSHKRPVDQDW 72
 QY 61 CCHAHDCCYGRLEKIGCPEKLYLFSVSRGIFCAAGRITCQRLTCEDKRALCPRNL 120
 Db 73 CCHAHDCCYGRLEKIGCPEKLYLFSVSRGIFCAAGRITCQRLTCEDKRALCPRNL 132
 QY 121 GTYNRKYAHYPNKLCTGPPTPC 142
 Db 133 GTYNRKYAHYPNKLCTGPPTPC 154

RESULT 4
 AAB2810
 ID AAB2810 standard; protein; 142 AA.
 XX
 AC AAB2810;
 XX 27-NOV-2000 (first entry)
 XX DE Mouse secretory type phospholipase A2 protein SEQ ID NO:15.
 XX KW Mouse; secretory phospholipase A2; PLA2; screening; development;
 XX inhibitor.
 OS Mus musculus.
 XX PN JP20000165568-A.
 XX PD 20-JUN-2000.
 PP 09-DEC-1998; 98JJP-00349604.
 PR 09-DEC-1998; 98JJP-00349604.
 PA (SHIO) SHIONOGI & CO LTD.
 DR WPI; 2000-4-85554/13.
 DR N-PSDB; AAA7130.
 PT New gene encoding mouse secretory type phospholipase A2 (PLA2) for
 XX screening for inhibitors of PLA2.

Claim 1; Page 13-14; 15pp; Japanese.

CC The present invention describes a mouse secretory type phospholipase A2 (PLA2) protein
 CC (PLA2) protein. The mouse secretory type PLA2-like protein can be used
 CC for screening in the development of inhibitors against the function of
 CC the protein. The present sequence represents mouse secretory type PLA2
 XX Sequence 142 AA;

Query Match 86.8%; Score 709; DB 3; Length 142;

Best Local Similarity 84.5%; Pred. No. 1.3e-57;
 Matches 120; Conservative 6; Mismatches 16; Indels 0; Gaps 0;
 QY 1 MKSPHVLVFLCLLYVALVGNLIVQFGVMIKEMTGKSAQLQNDYGCYCGIGGSHKRPVDQDW 60
 Db 1 MKPPIALACIICLVLPLAGGLVQFGVMIKEMTGKPAQLQNDYGCYCGIGGSHKRPVDQDW 60
 QY 61 CCHAHDCCYGRLEKIGCPEKLYLFSVSRGIFCAAGRITCQRLTCEDKRALCPRNL 120
 Db 61 CCHAHDCCYGRLEKIGCPEKLYLFSVSRGIFCAAGRITCQRLTCEDKRALCPRNL 120
 QY 121 GTYNRKYAHYPNKLCTGPPTPC 142
 Db 121 NTYNRKYAHYPNKLCTGPPTPC 142

RESULT 5
 AAB8101
 ID AAB8101 standard; protein; 142 AA.
 XX
 AC AAB8101;
 DT 12-JUN-2001 (first entry)
 XX Murine phospholipase A2 (PLA2) amino acid sequence.
 XX
 DE Phospholipase A2; PLA2; antibacterial; immunosuppressive; vulnerability;
 KW antiinflammatory; tranquiliser; antiasthmatic; antiallergic; trauma;
 KW antiinflammatory; antiarthritic; septic shock; pancreatitis; mouse;
 KW adult respiratory distress syndrome; ARDS; bronchial asthma;
 KW allergic rhinitis; rheumatoid arthritis.
 XX
 OS Mus musculus.
 XX
 Key Location/Qualifiers
 FH 1.19
 Peptide /label= Signal_Peptide
 FT 20..142
 Protein /label= Mature_PLA2
 FT /note= "Mature phospholipase A2"
 XX
 PN WO200121775-A1.
 XX
 PD 29-MAR-2001.
 XX
 PP 18-SEP-2000; 2000WO-JP000344.
 XX
 PR 21-SEP-1999; 99JJP-00266616.
 XX
 PA (SHIO) SHIONOGI & CO LTD.
 XX
 PT Ishizaki J, Suzuki N, Hanasaki K;
 XX
 WPI; 2001-290432/30.
 DR N-PSDB; AAF77387.
 XX
 PT Human secretory phospholipase A2 and encoded gene, useful in diagnosis of
 PT septic shock, adult respiratory distress syndrome and rheumatoid
 PT arthritis.
 XX
 PS Example 3; Page 42; 50pp; Japanese.
 XX
 CC This invention relates to human secretory phospholipase A2 (PLA2) protein
 CC and the gene encoding it. Inhibitors of phospholipase A2 have
 CC antibacterial, immunosuppressive; antiinflammatory; tranquilliser;
 CC antiasthmatic; antiallergic; antirheumatic; and antiarthritic
 CC activity. The PLA2 protein, gene and an anti-PLA2 antibody are useful in
 CC the diagnosis of PLA2 associated diseases e.g. septic shock, adult
 CC respiratory distress syndrome, pancreatitis, trauma, bronchial asthma,
 CC allergic rhinitis and rheumatoid arthritis. The present sequence
 CC represents murine PLA2. The murine PLA2 gene sequence is used in the
 CC invention for the identification and characterisation of the human PLA2

XX PR 21-DEC-1990; 90GB-00027917.
 XX (ICRL) IMPERIAL CHEM IND PLC.
 PA Hollis M, Needham MRC, Gooding C, Grosveld FG, Antoniou M;
 PI Hollis M, Needham MRC, Gooding C, Grosveld FG, Antoniou M;
 XX WPI: 1995-067096/05.
 DR Novel type III and IV low mol. wt. phospholipase A2 enzymes - from humans
 PT and rats, also nucleic acid sequences useful, e.g. for recombinant prodn.
 PT of enzymes, research into Batten's disease, etc.
 XX Disclosure: Fig 15, 160PP; English.
 PS Disclosure: Fig 15, 160PP; English.

XX DR HPLA2, HPLA2-10, was derived
 PT from human brain RNA by RACE-PCR. HPLA2-10 (AA63046) was characterized
 PT as a novel type of PLA2, type IV, on the basis of its Cys content in
 CC comparison with human PLA2 types I (AA63054) and II (AA63055) (Updated
 CC on 25-MAR-2003 to correct PN field.)
 XX Sequence 144 AA:
 SQ This sequence is encoded by the phospholipase A2 (PLA2) cDNA. The cDNA
 CC was amplified using the primer sequences given in ARQ 6310-1 by PCR from
 CC a human lung cDNA library. The cDNA sequence was used in the construction
 CC of an expression vector which further comprised a promoter and a dominant
 CC control region. This vector was used in an expression system comprising a
 CC mammalian cell transformed with the vector. This expression system could
 CC be used to prepare pharmacologically useful polypeptides eg. human growth
 CC hormone (HGH), granulocyte stimulating factor (G-CSF) and PLA2.
 CC and for gene therapy. The mammalian host comprises erythroid cells and a
 CC heterologous promoter.
 XX Sequence 144 AA:
 SQ Query Match 45.1%; Score 368.5; DB 2; Length 144;
 Best Local Similarity 52.1%; Pred. No. 3.2e-26;
 Matches 73; Conservative 12; Indels 9; Gaps 2;
 Qy 12 LLVALVT----GNYFGVMILEKMGK-SALQNDYGCYCGIGGSHWPyDQTWCC 62
 Db 5 LLLAVIMIFGILQAGNLYNFHRMKLTTGEAALSYGYGCHGVGRGSPKDATRCC 64
 Qy - 63 HAHDCCYGRDEKLGLGPBPKEKYLPSVSEGIFCGRRTICORLTCEDKRALCFRRNLT 122
 Db 65 VTHDCCYKRLEKRGCGTKEKYLPSVSEGIFCGRRTICORLTCEDKRALCFRRNLT 124
 RESULT 11
 ID ABR4433 standard; protein: 144 AA.
 DT 18-AUG-2003 (first entry)
 DE Human secreted group IIA phospholipase A2 (sPLA2) enzyme.
 XX Group IIP secreted phospholipase A2; sPLA2; phosphatidylglycerol; human;
 KW phosphatidylcholine; antibacterial; virucide; cytostatic; vasoactive;
 KW antiinflammatory; pulmonary; cardiotonic; chromosome 1p35; transgenic;
 KW enzyme.
 XX Homo sapiens.
 OS XX WO2003033689-A1.
 PN XX DR 12-OCT-2001; 2001WO-1B002407.
 PD 24-APR-2003.
 XX PP 12-OCT-2001; 2001WO-1B002407.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX PI Lazdunski M, Lambeau G, Valentin E;
 XX DR WPI: 2003-403216/38.
 XX Novel mammalian secreted group IIF secreted phospholipase A2, useful for
 PT preventing and treating bacterial and viral infections, and cancers.
 XX Disclosure: Fig 1, 33PP; English.
 PS XX The invention relates to a mammalian secreted group IIF secreted
 CC phospholipase A2 (sPLA2) (I), where the enzyme is Ca2+ dependent,
 CC maximally active at pH 7-8 and hydrolyzes phosphatidylglycerol versus
 PI Tischfield JA, Seilhamer JJ;

XX PR 15-JUL-1994; 94WD-US007926.
 XX PR 15-JUL-1993; 93US-00091941.
 PR 26-JUL-1993; 93US-00097354.
 XX (INDV) UNIV INDIANA FOUND.
 PA (INCY-) INCYTE PHARM INC.
 XX PI

CC phosphatidylcholine with a 15-fold preference. A pharmaceutical composition comprising (1) is useful for treating or preventing viral and bacterial infections, and cancers. A pharmaceutical composition containing compounds capable of inhibiting catalytic activity of (1), biologically active compounds that bind sPLA₂ receptors, or a compound that modulates cell proliferation, cell migration, contraction or apoptosis is useful for treating disease states or disorders involving group IIF sPLA₂, such as inflammatory disease, cancers, cardiac and brain ischaemia, acute lung injury, acute respiratory distress syndrome or Crohn's disease. Specific antibodies are useful for searching new secreted mammalian Group IIF sPLA₂ or the homologues of the enzyme in other mammals. The encoding polynucleotides and vectors are useful for transforming animals and establishing a line of transgenic animals. Sequences ABR44232-238 represent various human sPLA₂ enzymes used in alignment studies with the GIIF sPLA₂ enzyme.

XX Sequence 144 AA;

Query Match	Score 368.5;	DB 6;	Length 144;
Best Local Similarity	52.1%;	Pred. No. 3.2e-26;	
Matches	73;	Mismatches	2;
Qy	12 LLVALVT-----GNLYQFGMTEKMTGK-SALQVNNYGGCYGIGSSHWPVDQTDWYC	62	
Db	5 LLLAVIMIFGILQAHNLVNFRMKLITGREALSYGGYGHGVRGSPKDADRC	64	
Qy	63 HAHDCCYGRGLEKPLKEKYLFSVSERGIFCAGRITQORLTCEDCDRAALCFRRNLGT	122	
Db	65 VTHDCCYKRLEKRGCGTKEFLSYKPSNNSGRITCAQDSRSQLCBCECDRAATCFARNKTT	124	
Qy	123 YNRKYAHYPNKLCTGPTPPC	142	
Db	- 125 YNKKYQYYSNKHCRGSTPRC	144	

RESULT 12
ABP96807
ID → ABP96807 standard; protein; 144 AA.
XX AC ABP96807;

XX DT 05-JUN-2003 (first entry)
XX DE Human phospholipase A2 group IIA (synovial) SEQ ID NO:3.

KW Phospholipase A2 group IIA; synovial; antisense modulation; inflammation; phospholipase A2 group IIA inhibitor; phosphorothioate; antiinflammatory; antidiabetic; cytostatic; antipsoriatic; vaccine; gene therapy; cancer; psoriasis; diabetics; enzyme.
XX OS Homo sapiens.
XX PN WO200297133-A1.
XX PD 05-DEC-2002.
XX PF 21-MAY-2002; 2002WO-US016135.

XX PR 25-MAY-2001; 2001HS-00865866.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Bennett CF, Wyatt JR;
XX DR WPI; 2003-14495/13.
XX N-PSDB; ACC46906, ACC46921.

XX PT New compound that hybridizes with and inhibits the expression of phospholipase A2. Group IIA, useful for preparing a composition for treating or preventing inflammation, cancer, psoriasis or diabetes.
XX PS Example 13; Page 95-96; 135pp; English.

CC The present invention describes a compound (1) comprising (1) comprising 8-50 nucleobases which is targeted to a 5' untranslated region (UTR), coding, 3' UTR or intron region of a nucleic acid molecule encoding phospholipase A2, group IIA (synovial), where the compound specifically hybridizes with CC and inhibits the expression of phospholipase A2, group IIA (synovial).
CC Also described: (1) a composition comprising the compound and a carrier CC or diluent; (2) a method of inhibiting the expression of phospholipase CC A2, group IIA in cells or tissues; and (3) a method of treating an animal CC having a disease or condition associated with phospholipase A2, group IIA CC (synovial). (1) has antiinflammatory, antidiabetic, cytostatic and CC antipsoriatic activities, and can be used in vaccines and in Gene CC therapy. The compound (1) can be used for preparing a composition for CC treating or preventing inflammation, cancer, psoriasis or diabetes. The CC present sequence represents human phospholipase A2 group IIA (synovial), CC which is used in an example from the present invention
XX SQ Sequence 144 AA;

Query Match	Score 368.5;	DB 6;	Length 144;
Best Local Similarity	52.1%;	Pred. No. 3.2e-26;	
Matches	73;	Mismatches	2;
Qy	12 LLVALVT-----GNLYQFGMTEKMTGK-SALQVNNYGGCYGIGSSHWPVDQTDWYC	62	
Db	5 LLLAVIMIFGILQAHNLVNFRMKLITGREALSYGGYGHGVRGSPKDADRC	64	
Qy	63 HAHDCCYGRGLEKPLKEKYLFSVSERGIFCAGRITQORLTCEDCDRAALCFRRNLGT	122	
Db	65 VTHDCCYKRLEKRGCGTKEFLSYKPSNNSGRITCAQDSRSQLCBCECDRAATCFARNKTT	124	
Qy	123 YNRKYAHYPNKLCTGPTPPC	142	
Db	- 125 YNKKYQYYSNKHCRGSTPRC	144	

RESULT 13
AC ABU63123
ID ABU63123 standard; protein; 144 AA.
XX AC ABU63123;
XX DT 25-SEP-2003 (first entry)
XX DE Human group IIA secreted phospholipase A2.
XX KW Human; group IIA secreted phospholipase A2; virucide; antibacterial; cytostatic; antiinflammation; vasoactive; cerebroprotective; spia2;
KW phosphatidylglycerol hydrolysis; phosphatidylcholine hydrolysis;
KW viral infection; bacterial infection; cancer; inflammatory disease;
KW cardiac ischaemia; brain ischaemia; acute lung injury;
KW acute respiratory distress syndrome; Crohn's disease; enzyme.
XX OS Homo sapiens.
XX PN US2003073087-A1.
XX PR 11-OCT-2001; 2001US-00975456.
XX PD 17-APR-2003.
XX XX PR 11-OCT-2000; 2000US-0239491P.
XX PD 11-OCT-2001; 2001US-00975456.
XX PA (LAZD) LAZDUNSKI M.
PA (LAMB) LAMBEAU G.
PA (VAL) VALENTIN E.
XX PI Lazdunski M, Lambeau G, Valentin E;
XX DR WPI; 2003-567302/53.
XX PT New mammal secreted group IIF phospholipase A2 or nucleic acid, useful
PT for treating or preventing viral or bacterial infections, or cancers, or
PT screening inhibitors of the enzyme for treating e.g. inflammatory
PT

PT diseases or ischemia.
 XX Disclosure; Fig 1; 16pp; English.

PS The invention describes a mammalian secreted group IIF phospholipase A2 (sPLA2), which is Ca2+-dependent, maximally active at pH of about 7-8 and hydrolyses phosphatidylglycerol versus phosphatidylinoline with about 15-fold preference. The mammalian composition is useful for treating a nucleic acid, or a pharmaceutical composition is useful for treating bacterial infections, or cancers. The inhibitors of sPLA2 or a composition comprising sPLA2 inhibitors is useful for treating disease states or disorders involving Group IIF sPLA2, e.g., inflammatory diseases, cancer, cardiac and brain ischaemia, acute lung injury, acute respiratory distress syndrome, or Crohn's disease. The enzyme is also useful for screening various chemical compounds for treating these diseases. This is the amino acid sequence of human group IIA phospholipase A2 used to determine a consensus sequence for human sPLA2s.

XX Sequence 144 AA;

Query Match Score 368.5; DB 6; Length 144;	Best Local Similarity 52.1%; Pred. No. 3.2e-26;
Matches 12; Mismatches 46; Indels 9; Gaps 2;	Indels 9; Gaps 2;

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Qy   12  LIVLVTT--...GNYCQFGUNIEKXMTGK-SALQYNDYGCYCGIGGSHWPVDQDUWCC 62
Db    5  LLLAVIMFRLQHQLNPHRRIKLTTGEAALSQYGGCHGVRGSPKDADTRCC 64
Qy   63  HAHDCCYGRLEKLGEPKLEKYLPSVSRGIFCGRITCQLRTCECDKRAALCFRRNLGT 122
Db   ^  65  VTHDCCYKRLEKRGTKFLSYKSNSGSRITCAKQDSRSQLCEDAAATCFARNTT 124
Qy   123  YNRKYAHYPNKLCTGTPTPC 142
Db   -  125  YNKCYQQYSNKHCRGSTPRC 144

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RESULT 14
 ADB75501 ID ADB75501 standard; protein; 144 AA.

XX AC ADB75501;

XX DT 04-DEC-2003 (first entry)
 XX DE Prostate cancer marker protein.

XX KW Prostate; cancer; cytostatic; gene therapy; marker.
 XX OS Homo sapiens.
 XX PN WO2003009814-A2.

XX PD 06-FEB-2003.
 XX PF 25-JUL-2002; 2002WO-US023913.

XX PR 25-JUL-2001; 2001US-0307982P.
 PR 22-AUG-2001; 2001US-031356P.

PR 25-SEP-2001; 2001US-0325020P.
 PR 12-DEC-2001; 2001US-034746P.

PR 05-MAR-2002; 2002US-0362158P.
 XX (MILL-) MILLENNIUM PHARM INC.

XX PA Schlegel R, Monahan JB, Endge WO, Gannavarapu M, Gorbatcheva B;
 PI Hoersh S, Kamatkar S, Wonsley AM, Giatt K, Zhao X, Anderson D;

XX DR WPI; 2003-248033/24.
 XX PT New nucleic acid molecule, useful for diagnosing or treating prostate cancer.

XX PS Disclosure; SEQ ID NO 325; 99pp; English.

XX The invention relates to newly discovered cancer markers associated with the cancerous state of prostate cells. Also disclosed is a method of assessing whether a patient is afflicted with prostate cancer. The method of the invention involves assessing the level of expression of a marker in a prostate cancer by comparing the level of expression of the marker in a patient sample and the normal level of expression of the marker in a control non-prostate cancer sample, where a significant increase in the level of expression of the marker in the patient sample and the normal level indicates that the patient is afflicted with prostate cancer. Nucleic acids of the invention are useful for diagnosing or treating prostate cancer, and may be useful in gene therapy. Sequences given in ADB7557-ADB7563 represent marker cDNA and proteins. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 144 AA;
 XX Query Match Score 368.5; DB 7; Length 144;
 Best Local Similarity 52.1%; Pred. No. 3.2e-26;
 Matches 12; Mismatches 46; Indels 9; Gaps 2;

Query	12 LLVALVTT--...GNYCQFGUNIEKXMTGK-SALQYNDYGCYCGIGGSHWPVDQDUWCC 62	Score 45.1%;	Score 368.5;
Db	5 LLLAVIMFRLQHQLNPHRRIKLTTGEAALSQYGGCHGVRGSPKDADTRCC 64	Best Local Similarity 52.1%;	Best Local Similarity 52.1%;
Qy	63 HAHDCCYGRLEKLGEPKLEKYLPSVSRGIFCGRITCQLRTCECDKRAALCFRRNLGT 122	Matches 12; Conservatve 73;	Matches 12; Conservatve 73;
Db	65 VTHDCCYKRLEKRGTKFLSYKSNSGSRITCAKQDSRSQLCEDAAATCFARNTT 124	Mismatches 46;	Mismatches 46;
Qy	123 YNRKYAHYPNKLCTGTPTPC 142	Indels 9;	Indels 9;
Db	125 YNKCYQQYSNKHCRGSTPRC 144	Gaps 2;	Gaps 2;

RESULT 15
 ADE63560 ID ADE63560 standard; protein; 144 AA.

XX AC ADE63560;

XX DT 29-JAN-2004 (first entry)
 XX DE Human Protein P14555, SEQ ID NO 9504.

XX KW Human; pain; neuronal tissue; gene therapy; CCI;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spined nerve injury; SNI; Chung,
 XX Homo sapiens.
 XX OS Homo sapiens.
 XX PN WO2003016475-A2.

XX PD 27-FEB-2003.

XX PR 14-AUG-2002; 2002WO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346182P.

PR 26-NOV-2001; 2001US-0333347P.
 XX (GEHO) GEN HOSPITAL CORP.
 PA (FARBY) BAYER AG.

XX PI Woolf C, D'urso D, Befort K, Costigan M;
 XX DR WPI; 2003-248312/26.
 XX PT GENBANK; P14555.

XX PT New composition comprising two or more isolated polypeptides, useful for

preparing a medicament for treating pain in an animal.

Claim 1; Page: 1017pp; English.

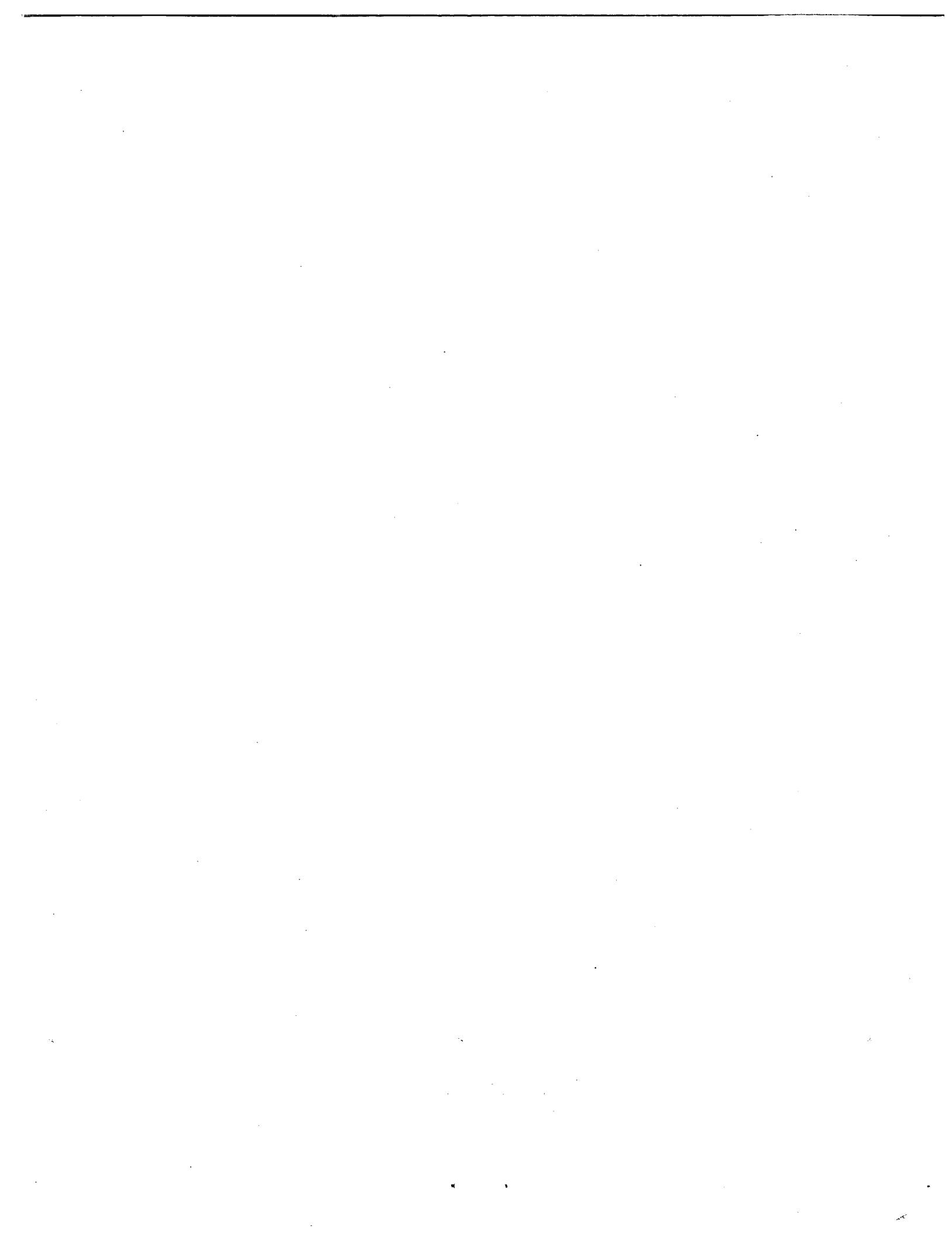
XX The invention discloses a composition comprising two or more isolated rat CC or human polynucleotides or a polynucleotide which represents a fragment, CC derivative or allelic variation of the nucleic acid sequence. Also CC claimed are a vector comprising the novel polynucleotide, a host cell CC comprising the vector, a method for identifying a polynucleotide sequence CC which is differentially regulated in an animal subjected to pain and a CC kit to perform the method, an array, a method for identifying an agent CC that increases or decreases the expression of the polynucleotide sequence CC that is differentially expressed in neuronal tissue of a first animal CC subjected to pain, a method for identifying a compound which regulates CC the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a CC compound that regulates the activity of one or more of the CC polynucleotides, a method for producing a pharmaceutical composition, a CC method for identifying a compound or small molecule that regulates the CC activity in an animal of one or more of the polypeptides given in the CC specification, a method for identifying a compound useful in treating CC pain and a pharmaceutical composition comprising the one or more CC polypeptides or their antibodies. The polynucleotide or the compound that CC modulates its activity is useful for preparing a medicament for treating CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene CC therapy). The sequence presented is a human protein (shown in Table 2 of CC the specification) which is differentially expressed during pain. Note: CC The sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic form directly from WIPO at CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ - Sequence 144 AA;

Qy	12	LLVALT-----GNIYQFGVMIKEKMGK-SALQNDYGGCYCGIGGSHWPVDQTDWCC
Db	5	LILLAVIMTEGLLQAHGNLYNFHMKIUTGKEAALSYFYGHCVGVRGSPXDAFRC
Qy	63	HAHDCCYGGLEKLGCEPKLEYLFSVSERGIFCAGRITIQORLTCECDKRAALCFRNLT
Db	65	VTHDCCYKREKLEKRGCGTKLSYKFSNSCSRITAKOSCRSOLCECDKAATTCFARNKT
Qy	123	YNRKYAHYFNKLCTGPTPRC 142
Db	125	YNKCYQYYSNKHCRGSTPRC 144

Query Match Similarity 45.1%; Score 368.5; DB 7; Length 144;
 Best Local Matches 52.1%; Pred. No. 3.2e-26; Mismatches 12; Indels 9; Gaps 2;

Search completed: July 3, 2004, 05:16:16
 Job time : 43.1887 secs



A; Note: this protein was also detected in platelets
 R.; Kramer, R.M.; Johansen, B.; Hession, C.; Pepinsky, R.B.
 Adv. Exp. Med. Biol. 275, 35-53, 1990
 A; Title: Structure and Properties of a secretable phospholipase A-2 from human platelets
 A; Reference number: A60266; MUID:91050834; PMID:2239446
 A; Accession: A60266
 A; Status: not compared with conceptual translation
 A; Residues: 1-144 <KR3>
 A; Molecule type: DNA
 A; Residues: 1-144 <SET>
 A; Cross-references: GB:J04704; EMBL:M22430; PIDN:9190888; PID:9190889
 R.; Schildknecht, J.J.; Pruzanski, W.; Vadas, P.; Miller, S.; Miller, J.A.; Kloss, J.; Johnson
 J. Biol. Chem. 264, 5335-5338, 1989
 A; Title: Cloning and recombinant expression of phospholipase A-2 present in rheumatoid a
 A; Reference number: A32847; MUID:9174566; PMID:2923608
 A; Accession: A32847
 A; Molecule type: mRNA
 A; Residues: 1-144 <SET>
 R.; Crowl, R.; Stoner, C.; Stoller, T.; Pan, Y.C.; Conroy, R.
 Adv. Exp. Med. Biol. 279, 173-184, 1990
 A; Title: Isolation and characterization of cDNA clones from human placenta coding for ph
 A; Reference number: A60363; MUID:91263879; PMID:1710870
 A; Accession: A60263
 A; Status: not compared with conceptual translation
 A; Molecule type: tRNA
 A; Residues: 1-144 <CR0>
 R.; Itoh, C.Y.; Wada, K.
 Biochem. Biophys. Res. Commun. 157, 488-493, 1988
 A; Title: Phospholipase A-2 from human synovial fluid: purification and structural homolo
 A; Reference number: A31150; MUID:89076274; PMID:3202859
 A; Accession: A31350
 A; Molecule type: protein
 A; Residues: 21-33 <SLA1>
 R.; Hara, S.; Kudo, I.; Matsuta, K.; Miyamoto, T.; Inoue, K.
 J. Biochem. 104, 326-328, 1988
 A; Title: Amino acid composition and NH2-terminal amino acid sequence of human phospholip
 A; Reference number: PR0056; MUID:89197814; PMID:3240982
 A; Molecule type: protein
 A; Residues: 21-46, 'X', 48-54 <HAR>
 R.; Kanda, A.; Ono, T.; Yoshida, N.; Tojo, H.; Okamoto, M.
 Biochem. Biophys. Res. Commun. 167, 42-48, 1989
 A; Title: The primary structure of a membrane-associated phospholipase A-2 from human spl
 A; Accession: A32913
 A; Molecule type: protein
 A; Residues: 21-144 <KAN>
 R.; Parks, T.P.; Lukas, S.; Hoffman, A.F.
 Adv. Exp. Med. Biol. 275, 55-81, 1990
 A; Title: Purification and characterization of a phospholipase A-2 from human osteoarthri
 A; Reference number: A60265; MUID:9105035; PMID:2146857
 A; Molecule type: protein
 A; Residues: 21-45, 'X', <PAR>
 R.; Recklies, A.D.; White, C.
 Arthritis Rheum. 34, 1106-1115, 1991
 A; Title: Phospholipase A-2 is a major component of the salt-extractable pool of matrix p
 A; Reference number: A61201; MUID:91050329
 A; Accession: A61201
 A; Molecule type: protein
 A; Residues: 21-40 <REC>
 R.; Green, J.A.; Smith, G.M.; Buchta, R.; Lee, R.; Ho, K.Y.; Rajkovic, I.A.; Scott, K.P.
 Inflammation 15, 355-361, 1991
 A; Title: Circulating phospholipase A-2 activity associated with sepsis and septic shock
 A; Reference number: A61634; MUID:92098137; PMID:1757123
 A; Accession: A61634
 A; Molecule type: protein
 R.; Werry, J.P.; Schevitz, R.W.; Clawson, D.K.; Bobbitt, J.L.; Dow, E.R.; Gamboa, G.; Good
 Teater, C.; Warrick, M.W.; Jones, N.D.
 A; Title: Structure of recombinant human rheumatoid arthritic synovial fluid phospholipase
 A; Contents: annotation; X-ray crystallography
 C; Genetix:
 A; Gene: PLAA2A; PLAA2B; PLAA2L
 A; Cross-references: GDB:PLAA2A; OMIM:172411
 A; Map Position: 1p16.1-1p35
 A; Introns: 14/1; 62/2; 98/1
 C; Function:
 A; Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-acyl
 A; Note: The reaction is strongly enhanced when the phospholipid is condensed into a mice
 C; Superfamily: phospholipase A
 C; Subfamily: phospholipase A ester hydrolase; extracellular protein; lipid degradation
 C; Keywords: calcium; carboxylic ester hydrolase; signal sequence #status predicted; <SG>
 F:1-20/Domain: signal sequence #status experimental <MAT>
 F:21-147/Product: phospholipase A2 IIIA #status experimental
 F:46-137; R:64-63-17; N:10-110-97-108/Dsulfide bonds: #status experimental
 F:47-49, 51-68/Binding site: calcium (His, GLY, GLY) #status predicted
 F:67,111/Active site: His, Asp #status predicted
 Query Match 49.9% Score 360.5; DB 1; Length 144;
 Best Local Similarity 55.6% Pred. No. 7-6e-28;
 Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;
 Qy 1 NLVQFVSMVTKMTRGK-SALQYNDGCGCYSWMPVDTDWCCHAHDCCYGRLEKIGCE 59
 Db 21 NLVNFERMIKLTGGEAISYGFVGCHGVGRGSPSKATDRCCVTHDCYCRLERKGCG 80
 Qy 60 PKEKYLFSYSERGIFCAAGRITTCORLTBCDCKRALCFPRNLGTYRNKAHYPNKLCTGP 119
 Db 81 TKFLSTKFNSGSRSRITCAKODSCRSQLCBDKAKATCFARNKTTYNKQIYFNSKHCGRS 140
 Db 120 TPPC 123
 Db 141 TPPC 144
 RESULT 3
 S13019
 Phospholipase A2 (EC 3.1.1.4) - horn viper
 C; Species: Cerastes cerastes (horn viper)
 C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
 C; Accession: S13019
 R.; Siddiqi, A.R.; Shatqat, J.; Zaidi, Z.H.; Joernvall, H.
 PEBS Lett. 278, 14-16, 1991
 A; Title: Characterization of phospholipase A2 from the venom of Horned viper (Cerastes ce
 A; Reference number: S13019; MUID:91130587; PMID:1993470
 A; Accession: S13019
 A; Status: Preliminary
 A; Molecule type: protein
 A; Residues: 1-120 <SID>
 C; Superfamily: phospholipase A2
 C; Keywords: carboxylic ester hydrolase
 Query Match 49.7% Score 358.5; DB 2; Length 120;
 Best Local Similarity 54.2% Pred. No. 1e-27; Mismatches 41; Indels 3; Gaps 2;
 Matches 64; Conservative 10;

Qy 1 NLVQFVSMVTKMTRGK-SALQYNDGCGCYSWMPVDTDWCCHAHDCCYGRLEKIGCE 59
 Db 1 NLVQFVSMVTKMTRGK-SALQYNDGCGCYSWMPVDTDWCCHAHDCCYGRLEKIGCE 59
 Qy 60 PKEKYLFSYSERGIFCAAGRITTCORLTBCDCKRALCFPRNLGTYRNKAHYPNKLCTGP 117
 Db 59 PKEKYLFSYSERGIFCAAGRITTCORLTBCDCKRALCFPRNLGTYRNKAHYPNKLCTGP 116
 R.; Werry, J.P.; Schevitz, R.W.; Clawson, D.K.; Bobbitt, J.L.; Dow, E.R.; Gamboa, G.; Good
 Teater, C.; Warrick, M.W.; Jones, N.D.
 A; Title: Structure of recombinant human rheumatoid arthritic synovial fluid phospholipase
 A; Contents: annotation; X-ray crystallography
 C; Genetix:
 A; Gene: PLAA2A; PLAA2B; PLAA2L
 A; Cross-references: GDB:PLAA2A; OMIM:172411
 A; Map Position: 1p16.1-1p35
 A; Introns: 14/1; 62/2; 98/1
 C; Function:
 A; Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-acyl
 A; Note: The reaction is strongly enhanced when the phospholipid is condensed into a mice
 C; Superfamily: phospholipase A
 C; Subfamily: phospholipase A ester hydrolase; extracellular protein; lipid degradation
 C; Keywords: calcium; carboxylic ester hydrolase; signal sequence #status predicted; <SG>
 F:1-20/Domain: signal sequence #status experimental <MAT>
 F:21-147/Product: phospholipase A2 IIIA #status experimental
 F:46-137; R:64-63-17; N:10-110-97-108/Dsulfide bonds: #status experimental
 F:47-49, 51-68/Binding site: calcium (His, GLY, GLY) #status predicted
 F:67,111/Active site: His, Asp #status predicted
 Query Match 49.9% Score 360.5; DB 1; Length 144;
 Best Local Similarity 55.6% Pred. No. 7-6e-28;
 Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;
 Qy 1 NLVQFVSMVTKMTRGK-SALQYNDGCGCYSWMPVDTDWCCHAHDCCYGRLEKIGCE 59
 Db 21 NLVNFERMIKLTGGEAISYGFVGCHGVGRGSPSKATDRCCVTHDCYCRLERKGCG 80
 Qy 60 PKEKYLFSYSERGIFCAAGRITTCORLTBCDCKRALCFPRNLGTYRNKAHYPNKLCTGP 119
 Db 81 TKFLSTKFNSGSRSRITCAKODSCRSQLCBDKAKATCFARNKTTYNKQIYFNSKHCGRS 140
 Db 120 TPPC 123
 Db 141 TPPC 144
 RESULT 4
 S22388
 phospholipase A2 (EC 3.1.1.4) ammodytin I2 precursor - western sand viper
 C; Species: Vipera ammodytes ammodytes (western sand viper)

C;Date: 07-Apr-1994 #sequence_revision 19-May-1994 #text_change 21-Jul-2000
 C;Sequence: S22388; S36686; S36655
 R;Krizaj, I.; Liang, N.S.; Burger, J.; Strukelj, B.; Ritonja, A.; Gubensek, F.
 Eur. J. Biochem. 204, 157-162, 1992
 A;Title: Amino acid and cDNA sequences of a neutral phospholipase A(2) from the long-nose
 A;Reference number: S22388; MUID:32201190; PMID:1551586
 A;Accession: S22388
 A;Molecule type: mRNA
 A;Cross-references: EMBL:X56678; PID:95702035; PIDN:CAA40200.2; PMID:95702036
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-137 <KR>
 R;Gubensek, F.
 Submitted to the EMBL Data Library, January 1991
 A;Reference number: S36685
 A;Accession: S36685
 A;Molecule type: mRNA
 A;Residues: 1-131 'S' 133-137 <GUB>
 A;Cross-references: EMBL:X56678; PID:9564450; PIDN:CAA40200.1; PMID:9644451
 C;Keywords: calcium binding; carboxylic ester hydrolase; venom
 F;1-16/Domain: signal sequence #status predicted <SIG>
 F;17-137/Domain: signal sequence #status Predicted <MAT>
 F;43-45,47-64/Binding site: ammonium [Tyr, Glu, Gly, Asp] #status predicted
 F;63,105/Active site: His, Asp #status Predicted
 Query Match Score 358; DB 2; Length 137;
 Best Local Similarity 54.8%; Pred. No. 1.3e-27;
 Matches 68; Conservative 11; Mismatches 41; Indels 4; Gaps 3;
 Qy : 1 NLVQFGVMIEKMTGKSA-LQYNDPGYCCTGGSHMPVOTDWCCHAHDCCYGRLEXLGCE 59
 Db 17 NLYQFGNMIFKMTKCSALIYSPTGCGWGGKPKQDADTRCCFVHDCYGRVN-GCD 74
 Qy : 60 PKEKYLPSYSERGIFCAGTTTCORLTCAKCDKAALCFERNLGTYNRKAHYPNLCTG 119
 Db 75 PKLSIYSSPENGDIVCGSDDPCLURAVCDRYAACFSEBNLNTDKYKNTYESSSHCT-E 133
 Qy 120 TPPC 123
 Db 134 TEQC 137
 RESULT 5
 B53872 Phospholipase A2 (EC 3.1.1.4) dimer - cottonmouth
 C;Species: Agkistrodon piscivorus (cottonmouth)
 C;Date: 26-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 24-Jul-1997
 C;Accession: B53872
 R;Welches, W.; Reardon, T.J.; Heindrikson, R.L.
 J. Protein Chem. 12, 187-193, 1993
 A;Title: An examination of structural interactions presumed to be of importance in the seric enzyme from the venom of Agkistrodon p. piscivorus.
 A;Reference number: A53872; MUID:93257049; PMID:8489705
 A;Contents: A. P. piscivorus
 A;Accession: B53872
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-123 <WEL>
 A;Experimental source: venom
 A;Note: Sequence extracted from NCBI backbone (NCBIP:132046)
 C;Superfamily: phospholipase A2
 C;Keywords: carboxylic ester hydrolase
 F;47,89/Active site: His, Asp #status Predicted
 Query Match Score 350; DB 2; Length 123;
 Best Local Similarity 52.0%; Pred. No. 6.9e-27;
 Matches 65; Conservative 14; Mismatches 42; Indels 4; Gaps 3;
 Qy : 1 NLVQFGVMIEKMTGKSA-LQYNDPGYCCTGGSHMPVOTDWCCHAHDCCYGRLEXLGCE 59

Db 1 NLFQFEKLRIKMTGKSGMLWISAYGGYCIGMGQQGGRPKDATDRCCFPVHDCYGRKV-TGCN 58
 Qy 60 PKEKYLPSYSERGIFCAGTTTCORLTCAKCDKAALCFERNLGTYNRKAHYPNLCTG 118
 Db 59 PGMIVTYSVDDNGNIVCGGTNPCKRQICECDRAAAICFRDNLKTYDSKTYWKPCRNCKE 118
 Qy 119 PPPC 123
 Db 119 BSEPC 123
 RESULT 6
 A33394 Phospholipase A2 (EC 3.1.1.4) precursor (version 1) - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 20-Jun-2000
 A;Accession: A33394; JUC031
 R;Ishizaki, J.; Ohara, O.; Nakamura, E.; Tamaki, M.; Ono, T.; Kanda, A.; Yoshida, N.; Ter Biochem. Biophys. Res. Commun. 162, 103-1036, 1989
 A;Title: cDNA cloning and sequence determination of rat membrane-associated phospholipase A1. Reference number: A33394; MUID:83350908; PMID:2164915
 A;Accession: A33394
 A;Molecule type: mRNA
 A;Residues: 1-166 <ISH>
 A;Cross-references: GB:W25148
 R;Komada, M.; Kudo, I.; Mizushima, H.; Kitamura, N.; Inoue, K.
 J. Biochem. 106, 545-547, 1989
 A;Title: Structure of cDNA coding for rat platelet phospholipase A2.
 A;Reference number: JU0131; MUID:90110043; PMID:2606907
 A;Accession: JU0131
 A;Molecule type: mRNA
 A;Residues: 1-166 <ROM>
 A;Cross-references: GB:D00523; NID:9220057; PIDN:BA000410.1; PMID:92200858
 C;Superfamily: phospholipase A2
 C;Keywords: phospholipase A2
 C;1-21/Domain: signal sequence #status predicted <SIG>
 F;22-146/Product: phospholipase A2 #status predicted <MAT>
 F;68,113/Active site: His, Asp #status Predicted
 Query Match Score 347; DB 2; Length 146;
 Best Local Similarity 51.2%; Pred. No. 1.6e-26;
 Matches 64; Conservative 14; Mismatches 45; Indels 2; Gaps 2;
 Qy : 1 NLVQFGVMIEKMTGKSA-LQYNDPGYCCTGGSHMPVOTDWCCHAHDCCYGRLEXLGCE 59
 Db 22 SLLERGMILFTKGKADVSFGYGGHCVGGRGSQRDADWCCVTHDCYGRKGCG 81
 Qy 60 PKEKYLPSYSERGIFCAGTTTCORLTCAKCDKAALCFERNLGTYNRKAHYPNLCTG 118
 Db 82 TKFLTKPFSYRGQIQISCTNGQSCRLQCCDKAALCFARNKSYSLKTYQFVPRFCKG 141
 Qy 119 PPPC 123
 Db 142 KTPSC 146
 RESULT 7
 PSBGAC Phospholipase A2 (EC 3.1.1.4) - horned viper
 N;Alternate names: caudoxin; Phosphatidylcholine 2-acylhydrolase
 C;Species: Bitis caudalis (horned viper)
 C;Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 24-Apr-1998
 C;Accession: A00762
 R;Viljoen, C.C.; Botes, D.P.; Kruger, H.
 Toxicon 20, 715-737, 1982
 A;Title: Isolation and amino acid sequence of caudoxin, a presynaptic acting toxic phospholipase A2. Reference number: A00762; MUID:63042262; PMID:7135414
 A;Molecule type: protein
 A;Residues: 1-121 <VIL>
 C;Comment: This enzyme is a presynaptic neurotoxin.

A;Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycerol-3-phosphocholine to 1-acyl-phospholipase A2 (EC 3.1.1.4) X - habu N:Alternate names: phosphatidylcholine 2-acylhydrolase C:Species: Trimeresurus flavoviridis (habu) C:Accession: A25500 R;Kini, R.M.; Kawabata, S.I.; Iwanaga, S. Toxicon, 24, 117-129, 1986. C:Function: Comparison of amino terminal region of three isoenzymes of phospholipases A2 (1) sequence of the basic phospholipase. TSV PL-X. A;Reference number: A94320; PMID:3564060 A;Accession: A25500 A;Molecule type: protein A;Residues: 1-122 <KIN> C:Function: catalyzes hydrolysis of 1,2-diacyl-sn-glycerol-3-phosphocholine to 1-acyl-phospholipase A2 C:Superfamily: phospholipase A2 A;Note: the reaction is strongly enhanced when the phospholipid is condensed into a mice C:Keywords: calcium, carboxylic ester hydrolase; homodimer; lipid degradation; metalloproteinase; F:25-122, 28-44, 43-95, 49-115, 50-88, 57-81, 75-86/Diester bonds: #status predicted F:27, 29, 31, 48/Binding site: calcium (Tyr, Gly, Asp) #status predicted F:47, 89/Active site: His, Asp #status predicted

Query Match Score 47.0%; Best Local Similarity 49.2%; Pred. No. 7.1e-26; Mismatches 16; Conservative 61; Matches 58; Gaps 3; Indels 44; Pairs 2;

Query Match Score 47.1%; Best Local Similarity 47.2%; Pred. No. 6.3e-26; Mismatches 15; Conservative 48; Matches 55; Gaps 1; Indels 2; Pairs 1;

Query Match Score 340; Best Local Similarity 47.2%; Pred. No. 6.3e-26; Mismatches 15; Conservative 48; Matches 55; Gaps 1; Indels 2; Pairs 1;

Query Match Score 340; Best Local Similarity 47.1%; Pred. No. 6.3e-26; Mismatches 15; Conservative 48; Matches 55; Gaps 1; Indels 2; Pairs 1;

Query Match Score 339.5%; Best Local Similarity 50.0%; Pred. No. 7.9e-26; Mismatches 15; Conservative 45; Matches 62; Gaps 3; Indels 44; Pairs 2;

Qy 1 NLVQFVMMIERTMGKSALQNDYCGYCIGGSHRPVDTDWCCCHAHDCCYGRLEKLGCPEP 60 Db 1 NLQFQNMISAMTGSLLATASYGYCGNGKGQEPDKDDRCCEVHDCCYGRADK--CSP 58 Qy 61 KLERKLFVSVERGIFCAGTTTCQRLTCEDKRAALCFRRNLGTYNRKYAHYPNKLCTGPT 120 Db 59 RMILYSYKPGHNTVCGDKRAACKRKVCECRVAACFAASKHSYNQNLWRYPPSSKCTGTA 118 Qy 121 PPC 123 Db 119 EKC 121

RESULT 8

PSTYAF phospholipase A2 (EC 3.1.1.4) X - habu N:Alternate names: phosphatidylcholine 2-acylhydrolase C:Species: Trimeresurus flavoviridis (habu) C:Accession: A25500 R;Kini, R.M.; Kawabata, S.I.; Iwanaga, S. Toxicon, 24, 117-129, 1986. C:Function: Comparison of amino terminal region of three isoenzymes of phospholipases A2 (1) sequence of the basic phospholipase. TSV PL-X. A;Reference number: A94320; PMID:3564060 A;Accession: A25500 A;Molecule type: protein A;Residues: 1-122 <KIN> C:Function: catalyzes hydrolysis of 1,2-diacyl-sn-glycerol-3-phosphocholine to 1-acyl-phospholipase A2 C:Superfamily: phospholipase A2 A;Note: the reaction is strongly enhanced when the phospholipid is condensed into a mice C:Keywords: calcium, carboxylic ester hydrolase; homodimer; lipid degradation; metalloproteinase; F:25-122, 28-44, 43-95, 49-115, 50-88, 57-81, 75-86/Diester bonds: #status predicted F:27, 29, 31, 48/Binding site: calcium (Tyr, Gly, Asp) #status predicted F:47, 89/Active site: His, Asp #status predicted

Query Match Score 47.0%; Best Local Similarity 49.2%; Pred. No. 7.1e-26; Mismatches 16; Conservative 61; Matches 58; Gaps 3; Indels 44; Pairs 2;

Query Match Score 340; Best Local Similarity 47.2%; Pred. No. 6.3e-26; Mismatches 15; Conservative 48; Matches 55; Gaps 1; Indels 2; Pairs 1;

Query Match Score 340; Best Local Similarity 47.1%; Pred. No. 6.3e-26; Mismatches 15; Conservative 48; Matches 55; Gaps 1; Indels 2; Pairs 1;

Query Match Score 339.5%; Best Local Similarity 50.0%; Pred. No. 7.9e-26; Mismatches 15; Conservative 45; Matches 62; Gaps 3; Indels 44; Pairs 2;

Qy 1 NLVQFVMMIERTMGKSALQNDYCGYCIGGSHRPVDTDWCCCHAHDCCYGRLEKLGCPEP 60 Db 1 NLQFQNMISAMTGSLLATASYGYCGNGKGQEPDKDDRCCEVHDCCYGRADK--CSP 58 Qy 61 KLERKLFVSVERGIFCAGTTTCQRLTCEDKRAALCFRRNLGTYNRKYAHYPNKLCTGPT 120 Db 59 RMILYSYKPGHNTVCGDKRAACKRKVCECRVAACFAASKHSYNQNLWRYPPSSKCTGTA 118 Qy 121 PPC 123 Db 119 EKC 121

RESULT 9

JC1342 phospholipase A2 (EC 3.1.1.4) Precursor - halys viper C:Species: Agkistrodon halys (halys viper) C:Accession: JC1342 R;Pan, H.; Cu-Yang, L.L.; Yang, G.Z.; Zhou, Y.C.; Wu, X.F.

Acta Biochim. Biophys. Sin. 28, 579-582., 1996 A;Title: Cloning of the BPLA2 gene from Agkistrodon halys Pallas. A;Reference number: JC1342 A;Contents: Snake venom A;Molecule type: mRNA A;Residues: 1-138 <PAN> A;Note: the authors translated the codon GAC for residue 54 as Asn C:Comment: This protein catalyzes specifically the hydrolysis of the C-2 ester bond of F:1-16/Domain: signal sequence #status predicted <SIG> F:17-138/Product: phospholipase A2 #status predicted <MAT>

C:Superfamily: phospholipase A2 C:Keywords: carboxylic ester hydrolase F:1-16/Domain: signal sequence #status predicted <SIG> F:17-138/Product: phospholipase A2 #status predicted <MAT>

Query Match Score 47.0%; Best Local Similarity 50.0%; Pred. No. 7.9e-26; Mismatches 15; Conservative 45; Matches 62; Gaps 3; Indels 44; Pairs 2;

Qy 1 NLVQFVMMIERTMGKSALQNDYCGYCIGGSHRPVDTDWCCCHAHDCCYGRLEKLGCPEP 60 Db 17 SLQFRKMIKMTGKEPPVSYAFGCGCGGSKPKDADTRCCFVHDCCYERL--TGCD 74 Qy 60 PKLEYLFVSVERGIFCAGTTTCQRLTCEDKRAALCFRRNLGTYNRKYAHYPNKLCTGPT 119 Db 75 PKWDDTYISKWGTIVCGGDDPCKKEVCECDKZAAICFRDLNLTKYKRYMTYFNLCSSK 134

RESULT 10

A35493 phospholipase A2 (EC 3.1.1.4) II precursor - rat C:Species: Rattus norvegicus (Norway Rat) C:Accession: A35493; S71310; R;Komada, M.; Kudo, I.; Inoue, K. Biochim. Biophys. Res. Commun. 168, 1059-1065, 1990 A;Title: Structure of gene coding for rat group II phospholipase A2. A;Reference number: A35493; MUID:30267443; PMID:2346480 A;Accession: A35493; MUID:90381322; PMID:2400792 A;Status: Preliminary A;Molecule type: DNA A;Cross-references: EMBL:X5127; PID:NAAA1223:1; PID:9204319 A;Note: the authors translated the codon TAT for residue 42 as Thr R;Kusunoki, C.; Satoh, S.; Kobayashi, M.; Niwa, M. Biochim. Biophys. Acta 1087, 95-97, 1990 A;Title: Structure of genomic DNA for rat platelet phospholipase A(2). A;Reference number: S71310; MUID:90381322; PMID:2400792 A;Accession: S71310 A;Molecule type: protein A;Residues: 1-146 <KIN> A;Molecule type: DNA A;Cross-references: EMBL:X5127; PID:NAAA1223:1; PID:9204319 A;Note: the authors translated the codon TAT for residue 42 as Thr R;Aarsman, A.J.; Schalkwijk, C.G.; Neys, P.W.; Iijima, N.; Werrett, J.R.; van den Bosch, R;Pan, H.; Cu-Yang, L.L.; Yang, G.Z.; Zhou, Y.C.; Wu, X.F.

Query Match Score 46.7%; Best Local Similarity 50.4%; Pred. No. 1.4e-25; Mismatches 14; Conservative 63; Matches 63; Gaps 2; C:Superfamily: phospholipase A2 C:Keywords: carboxylic ester hydrolase; lipid degradation F:68,113/Active site: His, Asp #status predicted

Qy 1 NLVQFVMMIERTMGKSALQNDYCGYCIGGSHRPVDTDWCCCHAHDCCYGRLEKLGCPEP 60 Db 1 NLQFQNMISAMTGSLLATASYGYCGNGKGQEPDKDDRCCEVHDCCYGRADK--CSP 58 Qy 60 PKLEYLFVSVERGIFCAGTTTCQRLTCEDKRAALCFRRNLGTYNRKYAHYPNKLCTGPT 119 Db 59 PKWXYTTSLENGDIVGGDPYCTRKVKBCKDKAICFRDLNLTKYKRYMTYFNLCSSK 134

RESULT 11

JC1342 phospholipase A2 (EC 3.1.1.4) Precursor - halys viper C:Species: Agkistrodon halys (halys viper) C:Accession: JC1342 R;Pan, H.; Cu-Yang, L.L.; Yang, G.Z.; Zhou, Y.C.; Wu, X.F.

RESULT 11

I50098 PKEKYLFSYSERGIFCA-GRTTCORLTBCDKRAALCPRNLTGTYNEKYAHYPNKLCTG 118
Species: Bothrops jararacussu ('jararacussu')
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 18-Jun-1999
C;Accession: I50098 ; S41247
R.;Moura-da-Silva, A.M.; Paine, M.J.; Diniz, M.R.; Theakston, R.D.; Crampton, J.M.
J.; Mol. Evol. 41: 174-179, 1995
A;Title: The molecular cloning of a phospholipase A2 from Bothrops jararacussu snake venom
A;Reference: I50098; MUID:95395872; PMID:7666446
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Cross-references: PLA-2
A;Gene: PLA-2
C;Superfamily: phospholipase A2
F;63,105/Active site: His, Asp #status predicted

Query Match Score 335.5; DB: 2; Length 138;
Best Local Similarity 50.0%; Pred. No. 1.0e+25;
Matches 62; Conservative 12; Mismatches 47; Indels 3; Gaps 2;

Qy * 1 NLVQFGVMERMTGKSAL-QYNDYGGSHWPVQDTCWCHANDCCYGRLEKGCE 59
Db 17 DLWQFGMQLIKEKTLGKPLPPFYTYTRGCGGCCQGPXDATDRCCFVHDCCYSKL--TNCK 74

Qy 60 PKEKYLFSYSERGIFCA-RTTTCORLTBCDKRAALCPRNLTGTYNEKYAHYPNKLCTG 119
Db 75 PKTDRSYRENGVIIQGGTPECEQKICECDRAAVCFRNLRYKRYMAXPDVLCKKP 134

Qy 120 TPPC 123
Db 135 AEKC 138

RESULT 12

I48342 PKEKYLFSYSERGIFCA-RTTTCORLTBCDKRAALCPRNLTGTYNEKYAHYPNKLCTG 118
Species: Mus musculus ('house mouse')
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
C;Accession: I48342; PC2009; S3548; I49352
R.;Mulherkar, R.; Rao, R.S.; Wagle, A.S.; Patki, V.; Deo, M.G.
Biochem. Biophys. Res. Commun. 195, 1254-1263, 1993
A;Title: Enhancing factor, a Paneth cell specific protein from mouse small intestines: I
A;Reference number: I48342; MUID:94029955; PMID:8267667
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Cross-references: mRNA
A;Residues: 1-146 <MUL1>
A;Molecule type: mRNA
A;Note: Correction of S35948
R.;Mulherkar, R.; Rao, R.S.; Wagle, A.S.; Patki, V.; Deo, M.G.
Biochem. Biophys. Res. Commun. 197, 351-352, 1993
A;Title: Enhancing factor, a peneth cell specific protein from mouse small intestines: I
A;Accession: PC2009
A;Molecule type: mRNA
A;Residues: 22-146 <MUL2>

submitted to the EMBL Data Library, July 1993
A;Reference number: S35948
A;Accession: S35948
A;Molecule type: mRNA
A;Residues: 22-115, R' 118-146 <MUL3>
A;Cross-references: EMBL:X74266
R.;Kennedy, B.P.; Parrette, P.; Mudgett, J.; Vadas, P.; Pruzanski, W.; Kwan, M.; Tang, C.; Biol. Chem. 270, 22378-22385, 1995
A;Title: A natural distribution of the secretory group II phospholipase A2 gene in inbred n
A;Reference number: I49352
A;Accession: I49352
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-18, V, '20-85, 'K', 87-146 <KEN>
A;Cross-references: EMBL:U3238; NID:94836; PIDN: AAC52252.1; PID:9984837
C;Superfamily: phospholipase A2
C;Keywords: carboxylic ester hydrolase
F;68,113/Active site: His, Asp #status predicted

Query Match Score 335.5; DB: 2; Length 146;
Best Local Similarity 52.0%; Pred. No. 2.3e-25;
Matches 65; Conservative 9; Mismatches 49; Indels 2; Gaps 2;

Qy 1 NLVQFGVMERMTGKSAL-QYNDYGGSHWPVQDTCWCHANDCCYGRLEKGCE 59
Db 22 NIAQFSEMIRLKTKGAEELSTAFYGCGLGGKSPKDADRCCTVTHDCYKSLEKSGCG 81

Qy 60 PRLEYKLFSSYSERGIFCA-AGRFTTCORLTCECDKRALCFFRNLCYAHYPNKLCTG 118
Db 82 TKLLTKYKSHOGQQTCSANONSQCRLCQCDDKAACECFARNKKTYSLKIQFYPNMFCKG 141

Qy 119 TPPC 123
Db 142 KKPKC 146

RESULT 13

A25806 PKEKYLFSYSERGIFCA-AGRFTTCORLTCECDKRALCFFRNLCYAHYPNKLCTG 118
Species: phospholipase A2 (EC 3.1.1.4) B - western sand viper
NA;Alternative names: ammodytoxin B
C;Species: Vipera ammodytes (western sand viper)
C;Date: 05-Jun-1988 #sequence_revision 05-Jun-1998 #text_change 28-Aug-1998
R.;Ritonja, A.; Machleidt, W.; Turk, V.; Gubensek, F.
Biol. Chem. Hoppe-Seyler 367, 919-923, 1986
A;Title: Amino-acid sequence of ammodytoxin B partially reveals the location of the site
A;Reference number: A25806; MUID:87076055; PMID:3790259
A;Accession: A25806
A;Molecule type: protein
A;Residues: 1-122 <KIT>
C;Superfamily: phospholipase A2
C;Keywords: carboxylic ester hydrolase
F;26-115,28-44-43-95,49-122,50-88,57-81,75-86/Disulfide bonds: #status predicted
F;47,59/Active site: His, Asp #status predicted

Query Match Score 333.5; DB: 2; Length 122;
Best Local Similarity 47.6%; Pred. No. 2.7e-25;
Matches 59; Conservative 18; Mismatches 44; Indels 3; Gaps 2;

Qy 1 NLVQFGVMERMTGKSAL-QYNDYGGSHWPVQDTCWCHANDCCYGRLEKGCE 59
Db 1 SLLEFMMILGETGKPLTSYSFIGCYCGGGKSPKDADRCCTVTHDCYFNMFCKG 81

Qy 60 PRLEYKLFSSYSERGIFCA-AGRFTTCORLTCECDKRALCFFRNLCYAHYPNKLCTG 119
Db 59 PKTDRKYHRENGVIVCGKGTSCRNICECDRAAACFRKNLXKTYHMYYPDFLCKKB 118

Qy 120 TPPC 123
Db 119 SEKC 122

RESULT 14

S10333
ammodytoxin B precursor - sand viper
C;Species: Vipera ammodytes (sand viper)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999
C;Accession: S10333
R;Kordis, D.; Pungorcar, J.; Strukelj, B.; Liang, N.; Gubensek, F.
Nucleic Acids Res. 18, 4016, 1990
A;Title: Sequence of the cDNA coding for ammodytoxin B;
A;Reference number: S10333; MUID:90326552; PMID:2374735
A;Accession: S10333
A;Status: Preliminary
A;Molecule type: mRNA
A;Residues: 1-138 <KOR>
A;Cross-references: EMBL:X52241; NID:964441; PID:CAA36486.1; PID:964442
C;Superfamily: phospholipase A2
C;Conservation: Superfamily A2

Query Match 46.2%; Score 333.5; DB 2; Length 138;
Best Local Similarity 47.6%; Pred. No. 3e-25; Indels 3; Gaps 2;
Matches 59; Conservative 18; Mismatches 44; Indels 3; Gaps 2;

Qy 1 NLVQGVMTGKSAI-QNDYGCYCGIGSHWPVQDTDWCHAHDCGYBLEKGCE 59
Db 17 SLLERGMIMGETGKVNPLTSYSFGCYCGVGGKGTPKDATDRCFVHDCCGNLP--DCS 74

Qy 60 PKLEYLFYSVERGIFCAAGRITCORLTICPKEAALCFRRNLGTYNKRYAHYPNKLCTG 119
Db 75 PTKDRYKIHRENGAIVGKGTSCENRICBDRAAAICFRKNLKTYNHIMYPDFLCKKE 134

Qy 120 TPPC 123
Db 135 SEKC 138

RESULT 15

JU0283
phospholipase A2 (EC 3.1.1.4) precursor (version 2) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 24-Jul-1997
C;Accession: JU0283
R;Komada, M.; Kudo, I.; Mizushima, H.; Kitamura, N.; Inoue, K.
J. Biochem. 106, 545-547, 1989
A;Title: Structure of cDNA coding for rat platelet phospholipase A2.
A;Reference number: JU0131; MUID:90110043; PMID:2608907
A;Accession: JU0283
A;Molecule type: mRNA
A;Residues: 1-146 <KOM>
C;Superfamily: phospholipase A2
C;Keywords: carboxylic ester hydrolase
F;1:21/Domain: signal sequence #status Predicted <SIG>
F;2:146/Product: phospholipase A2 #status Predicted <MAT>
F;6;1113/Active site: His, Asp #status Predicted
A;Cross-references: EMBL:X52241; NID:964441; PID:CAA36486.1; PID:964442
C;Conservation: Superfamily A2

Query Match 46.1%; Score 333; DB 2; Length 146;
Best Local Similarity 49.6%; Pred. No. 3.5e-25; Indels 2; Gaps 2;
Matches 62; Conservative 14; Mismatches 47; Indels 2; Gaps 2;

Qy 1 NLVQGVMTGKSAI-LQYNDYGCYCGIGSHWPVQDTDWCHAHDCGYBLEKGCE 59
Db 22 SLLERGMIMGETGKVNPLTSYSFGCYCGVGGKGTPKDATDRCFVHDCCGNLP--DCS 81

Qy 60 PKLEYLFYSVERGIFCA-GRITTCORLTICPKEAALCFRRNLGTYNKRYAHYPNKLCTG 118
Db 82 TKEYLYKFSPRGQQIASCNTQDSRKQLSCDVAEEFBNKSYSLKQFYPNKEFKG 141

Qy 119 PTTPPC 123
Db 142 KTPSC 146

Result No.	Score	Query	Match	Length	DB	ID	Description
-	-	-	-	-	-	-	-
-	1	PA2E_HUMAN	PA2E_HUMAN	142	1	P244294	eristocophi
-	2	PA2E_MOUSE	PA2E_HUMAN	91.7	1	P42192	agkistrodon
-	3	PA2A_ERIMA	PA2E_HUMAN	51.5	1	Q92147	trimeresuru
-	4	PA2A_HUMAN	PA2E_HUMAN	49.9	1	PA2P_TRAFL	PA2P-TRIFL
-	5	PA2A_CERCE	PA2E_HUMAN	49.7	1	P47711	echis ocelli
-	6	PA2N_VTPAA	PA2E_HUMAN	49.6	1	P59171	cavia porce
-	7	dabola	PA2E_HUMAN	49.2	1	PA25_TRAFL	PA25-TRIGA
-	8	PA2D_DABRR	PA2E_HUMAN	48.5	1	P42190	agkistrodon
-	9	PA2I_AKGPI	PA2E_HUMAN	48.1	1	PA26_AKGHP	PA26_AKGHP
-	10	PA2A_RAT	PA2E_HUMAN	47.7	1	P47711	cavia porce
-	11	PA2Y_TRAFL	PA2E_HUMAN	47.2	1	PA23_AKGHP	PA23_AKGHP
-	12	PA2A_MOUSE	PA2E_HUMAN	47.2	1	P14421	agkistrodon
-	13	PA2A_TRAFL	PA2E_HUMAN	47.2	1	PA21_TRAFL	PA21_TRAFL
-	14	PA2A_BITCA	PA2E_HUMAN	47.1	1	P06862	trimeresuru
-	15	PA2X_TRAFL	PA2E_HUMAN	47.0	1	P06860	trimeresuru
-	16	PA2A_AKGHP	PA2E_HUMAN	46.9	1	P14424	vipera ammo
-	17	PA2B_VIPPA	PA2E_HUMAN	47.0	1	P59071	dabola russus
-	18	PA29_AKGHP	PA2E_HUMAN	46.9	1	P00249	agkistrodon
-	19	PA2B_TRAFL	PA2E_HUMAN	46.9	1	P59265	trimeresuru
-	20	PA2W_TRAFL	PA2E_HUMAN	46.7	1	Q0517	trimeresuru
-	21	PA21_BOTUR	PA2E_HUMAN	46.5	1	P45881	bothrops ja
-	22	PA2A_VIPPA	PA2E_HUMAN	46.3	1	P00088	trimeresuru
-	23	PA2B_VIPPA	PA2E_HUMAN	46.2	1	P14424	vipera ammo
-	24	PA28_DABRR	PA2E_HUMAN	46.1	1	P59071	dabola russus
-	25	PA22_AKGHP	PA2E_HUMAN	46.1	1	P00249	agkistrodon
-	26	PA2A_VIPBB	PA2E_HUMAN	46.1	1	P31854	vipera berus
-	27	PA2A_VIPPA	PA2E_HUMAN	45.8	1	P00626	bothrops ja
-	28	PA2C_VIPPA	PA2E_HUMAN	45.8	1	P14047	vipera ammo
-	29	PA22_TRAFL	PA2E_HUMAN	45.6	1	P81478	trimeresuru
-	30	PA21_AKGHP	PA2E_HUMAN	45.5	1	P04117	agkistrodon
-	31	PA22_TRAFL	PA2E_HUMAN	45.4	1	Q8149	trimeresuru
-	32	PA21_TRAFL	PA2E_HUMAN	45.2	1	P24427	eristocophi
-	33	PA2A_TRAFL	PA2E_HUMAN	45.2	1	P90w39	trimeresuru

Scoring table: BL2USUM52
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
-	-	-	-	-	-	-	-
-	1	PA2E_HUMAN	PA2E_HUMAN	142	1	Qinz2	homo sapiens
-	2	PA2E_MOUSE	PA2E_HUMAN	91.7	1	Q9gl3	mus musculus
-	3	PA2A_ERIMA	PA2E_HUMAN	51.5	1	P24293	eristocophi
-	4	PA2A_HUMAN	PA2E_HUMAN	49.9	1	P14555	homo sapiens
-	5	PA2B_CERCE	PA2E_HUMAN	49.7	1	P21789	cerastes cerastes
-	6	PA2N_VTPAA	PA2E_HUMAN	49.6	1	P34180	vipera ammo
-	7	PA2D_DABRR	PA2E_HUMAN	49.2	1	P81458	dabola russus
-	8	PA2I_AKGPI	PA2E_HUMAN	48.5	1	P1972	agkistrodon
-	9	PA2A_RAT	PA2E_HUMAN	48.1	1	P14423	rattus norvegicus
-	10	PA2Y_TRAFL	PA2E_HUMAN	47.7	1	Q81470	trimeresurus
-	11	PA2A_MOUSE	PA2E_HUMAN	47.2	1	Q9Y777	trimeresurus
-	12	PA2A_MOUSE	PA2E_HUMAN	47.2	1	P14482	mus musculus
-	13	PA2A_TRAFL	PA2E_HUMAN	47.2	1	P59264	trimeresurus
-	14	PA2A_BITCA	PA2E_HUMAN	47.1	1	P06862	bitis cauda
-	15	PA2X_TRAFL	PA2E_HUMAN	47.0	1	P06860	trimeresurus
-	16	PA2A_AKGHP	PA2E_HUMAN	47.0	1	P142187	agkistrodon
-	17	PA2B_VIPPA	PA2E_HUMAN	47.0	1	Q3yqj7	vipera palau
-	18	PA29_AKGHP	PA2E_HUMAN	46.9	1	P42188	agkistrodon
-	19	PA2B_TRAFL	PA2E_HUMAN	46.9	1	P59265	trimeresurus
-	20	PA2W_TRAFL	PA2E_HUMAN	46.7	1	Q0517	trimeresuru
-	21	PA2A_VIPBB	PA2E_HUMAN	46.5	1	P45881	bothrops ja
-	22	PA2C_VIPPA	PA2E_HUMAN	46.3	1	P00088	trimeresuru
-	23	PA2B_VIPPA	PA2E_HUMAN	46.2	1	P14424	vipera ammo
-	24	PA28_DABRR	PA2E_HUMAN	46.1	1	P59071	dabola russus
-	25	PA22_AKGHP	PA2E_HUMAN	46.1	1	P00249	agkistrodon
-	26	PA2A_VIPBB	PA2E_HUMAN	46.1	1	P31854	vipera berus
-	27	PA2A_VIPPA	PA2E_HUMAN	45.8	1	P00626	bothrops ja
-	28	PA2C_VIPPA	PA2E_HUMAN	45.8	1	P14047	vipera ammo
-	29	PA22_TRAFL	PA2E_HUMAN	45.6	1	P81478	trimeresuru
-	30	PA21_AKGHP	PA2E_HUMAN	45.5	1	P04117	agkistrodon
-	31	PA22_TRAFL	PA2E_HUMAN	45.4	1	Q8149	trimeresuru
-	32	PA21_TRAFL	PA2E_HUMAN	45.2	1	P24427	eristocophi
-	33	PA2A_TRAFL	PA2E_HUMAN	45.2	1	P90w39	trimeresuru

ALIGNMENTS

RESULT 1

PA2E_HUMAN

ID PA2E_HUMAN STANDARD PRT; 142 AA.

AC Q9NZK7;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-Oct-2003 (Rel. 42, Last annotation update)

DE Group IIE secretory phospholipase A2 precursor (EC 3.1.1.4) (Phosphatidylcholine 2-acetylhololase GILE) (GIIIE SPLA2) (SPLA2) (IIE).

GN PLA2GE.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID:9606;

RN [1] FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2'-acyl groups in 3-sn-phosphoglycerides. Has a preference for arachidonic-containing phospholipids.

CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1- acylglycerophosphocholine + a fatty acid anion.

CC -1- COFACTOR: Binds 1 calcium ion per subunit.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Restricted to the brain, heart, lung, and placenta.

CC -1- SIMILARITY: Belongs to the phospholipase A2 family.

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CC DR EMBL_AF199279;AAF6541;1; -.

DR HSSP_P14555;1;POD.

DR PRODn; PDD0033; PhospholipaseA2.

DR GO; GO:0004624; F:secreted phospholipase A2 activity; TAS.

DR SMART; SM00085; PA2C; 1.

DR GO; GO:0006954; P:inflammatory response; TAS.

DR PROSITE; PS00119; PA2_ASPE; FALSE_NEG.

DR InterPro; IPR01211; PhospholipaseA2.

DR Pfam; PF00068; Phoslip; 1.

DR PRINTS; PR03883; PHOSPHOLIPASEA2.

DR PRODn; PDD0033; PhospholipaseA2; 1.

DR SMART; SM00085; PA2C; 1.

DR GO; GO:0006644; P:phospholipid metabolism; TAS.

DR PROSITE; PS00119; PA2_HIS; 1.

DR Hydrolase; Lipid degradation; Signal; Calcium.

FT SIGNAL 1 19

FT CHAIN 20 142

GROUP IIE SECRETORY PHOSPHOLIPASE A2.

FT	ACT_SITE	65	65	BY SIMILARITY.	CC	levels in various other tissues.
FT	ACT SITE	109	109	BY SIMILARITY.	CC	-!- SIMILARITY: Belongs to the phospholipase A2 family.
FT	DISULFID	44	135	BY SIMILARITY.	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
FT	DISULFID	46	62	BY SIMILARITY.	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
FT	DISULFID	61	115	BY SIMILARITY.	CC	the European Bioinformatics Institute. There are no restrictions on its
FT	DISULFID	67	142	BY SIMILARITY.	CC	use by non-profit institutions as long as its content is in no way
FT	DISULFID	68	108	BY SIMILARITY.	CC	modified and this statement is not removed. Usage by and for commercial
FT	DISULFID	77	101	BY SIMILARITY.	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to licensee@isb-sib.ch).
FT	DISULFID	95	106	BY SIMILARITY.	CC	
FT	METAL	45	45	CALCIUM (VIA CARBONYL OXYGEN)	CC	
FT	METAL	47	47	(VIA CARBONYL OXYGEN)	CC	
FT	METAL	49	49	CALCIUM (VIA CARBONYL OXYGEN)	CC	
FT	SEQUENCE	66	66	(BY SIMILARITY).	CC	
SQ	SEQUENCE	142 AA;	15989 MW;	3C360EA710E41FB CRC64;	CC	
Query Match		100.0% ; Best Local Similarity	Score 722; Pred. No. 5	Length 142; 4e-71;	CC	
Matches	122; Conservative	0; Mismatches	0;	Indels 0; Gaps 0;	CC	
Qy		1 NLVQFSVMTKMTGKSALQNDYGCYCGIGGSHPVDOTDWCCCHAHDCCYGRLEKLGCEP	60	FT SIGNAL 1	CC	GROUP IIE SECRETORY PHOSPHOLIPASE A2.
Db		20 NLVQFSVMTKMTGKSALQNDYGCYCGIGGSHPVDOTDWCCCHAHDCCYGRLEKLGCEP	60	FT CHAIN 20	CC	
Qy		61 KLEKYLFSVSERGIFCAGRITTCORLTCECDKRAALCFRRNLGTYNRKAYHYNPKLCCTGPT	120	FT ACT SITE 65	CC	
Db		80 KLEKYLFSVSERGIFCAGRITTCORLTCECDKRAALCFRRNLGTYNRKAYHYNPKLCCTGPT	139	FT DISTULFID 65	CC	
Qy		121 PPC 123		FT DISTULFID 65	CC	
Db		140 PPC 142		FT DISTULFID 68	CC	
RESULT 2				FT DISTULFID 68	CC	
PAGE_MOUSE				FT DISTULFID 70	CC	
ID	PA2E MOUSE	STANDARD;	PRT;	FT DISTULFID 77	CC	
AC	Q9QUL3 ;		14 AA.	FT DISTULFID 77	CC	
DT	28-FEB-2003 (Rel. 41, Created)			FT METAL 45	CC	
DT	28-FEB-2003 (Rel. 41, Last sequence update)			FT METAL 49	CC	
DT	10-OCT-2003 (Rel. 42, Last annotation update)			FT SEQUENCE 142 AA;	CC	
DE	Group IIE secretory phospholipase A2 precursor (EC 3.1.1.4)			66	CC	
DE	(Phosphatidylcholine 2-acetylhydrolase GIE) (GIE SPLA2) (SPLA(2)-IIE).			15942 MW;	CC	
GN	PLA2E.			8B0E3CC710A1F946 CRC64;	CC	
OS	Mus musculus (Mouse).			Query Match	CC	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			Best Local Similarity 91.7%; Score 662;	CC	
OC	Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.			Pred. No. 1.6e-64;	CC	
OX	NCBI_TaxID=10090;			Matches 109; Conservative 6;	CC	
RN	SEQUENCE FROM N.A.			Mismatches 0; Gaps 0;	CC	
RP	SEQUENCE FROM BALB/C;				CC	
RC	SEQUENCE FROM N.A., AND CHARACTERIZATION.				CC	
RX	MEDLINE=20148788; PubMed=10601567;				CC	
RA	Suzuki N., Ishizaki J., Yokota Y., Higashino K., Ono T., Ikeda M.,			RESULT 3	CC	
RA	Fujii N., Kawamoto K., Hanasaki K.,			PA21_BRIMA STANDARD;	CC	
RT	"Structures, enzymatic properties, and expression of novel human and			AC P2429;	CC	
RT	mouse secretory phospholipase A(2)s.";			ID 01-MAR-1992 (Rel. 21, Created)	CC	
RL	J. Biol. Chem. 275:5785-5793 (2000).			ID 01-MAR-1992 (Rel. 21, Last sequence update)	CC	
CC	"On the diversity of secreted phospholipases A2. Cloning, tissue distribution, and functional expression of two novel mouse group II enzymes".			DT 10-OCT-2003 (Rel. 42, Last annotation update)	CC	
CC	J. Biol. Chem. 274:31195-31202 (1999).			DE Phospholipase A2 isozyome PLA-1 (EC 3.1.1.4) (Phosphatidylcholine	CC	
[2]				-2-acetylhydrolase).	CC	
RN	SEQUENCE FROM N.A., AND CHARACTERIZATION.			DE Bristocophis macmahoni (Leaf-nosed viper).	CC	
RC	SEQUENCE FROM BALB/C;			OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	CC	
RX	MEDLINE=20148788; PubMed=10601567;			OC Lepidossauria; Squamata; Scleroglossa; Serpentes; Colubroidea.	CC	
RA				OC Viperidae; Viperinae; Eristocophis.	CC	

RA Lai C.Y., Wada K.; from human synovial fluid; purification and
RT structural homology to the placental enzyme.".
RL Biochem. Biophys. Res. Commun. 157:488-493 (1988).
RN [8]
SEQUENCE OF 21-75.
RP TISSUE=ileal mucosa;
RC MEDLINE=91002200; PubMed=8399335;
RX Minami T., Tojo H., Shiomura Y., Matsuzawa Y., Okamoto M.;
RA "Purification and characterization of a phospholipase A2 from human
RT ileal mucosa."
RT Biochim. Biophys. Acta 1170:125-130 (1993).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=91287926; PubMed=2052381;
RA Werry J.-P., Schevitz R.W., Clawson D.K., Bobbitt J.L., Dow E.R.,
RA Gamboa G., Goodson T. Jr., Kramer R.M., McClure D.B.,
RA Mierlich E.D., Putram J.E., Sharp J.D., Stark D.H., Teater C.,
RA Jones N.D.;
RT "Structure of recombinant human rheumatoid arthritic synovial fluid
phospholipase A2 at 2.2-A resolution.";
RT Nature 352:79-82 (1991).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=92054586; PubMed=1948070;
RA Scott D.J., White S.P., Browning J.L., Rosa J.J., Gelb M.H.,
RA Sigler P.B.;
RT "Structures of free and inhibited human secretory phospholipase A2
from inflammatory exudate";
RT RL Science 254:1007-1010 (1991).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=95139225; PubMed=7664108;
RA Schevitz R.W., Bach N.J., Carlson D.G., Chirgadze N.Y., Clawson D.K.,
RA Dillkard R.D., Drahein S.E., Hartley L.W., Jones N.D., Mihelich E.D.,
RA Olkowski J.J., Snyder D.W., Dand S.C., Werry J.-P.
RT "Structure-based design of the first potent and selective inhibitor
of human non-pancreatic secretory phospholipase A2.".
RT Nat. Struct. Biol. 2:458-465 (1995).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=98207049; PubMed=9530252;
RA Kitadokoro K., Hagaishiita S., Sato T., Ohtani M., Miki K.;
RT "Crystal structure of human secretory phospholipase A2-IIA complex
with the potent ionolizine inhibitor 120-1032.";
RL J. Biochem. 123:619-623 (1998).
CC -!- FUNCTION: Thought to participate in the regulation of the
phospholipid metabolism in biomembranes including eicosanoid
biosynthesis. Catalyzes the calcium-dependent hydrolysis of the 2-
acyl groups in 3-sun-phosphoglycerides.
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
acetylglycerophosphocholine + a fatty acid anion.
CC -!- COPACITOR: Binds 1 calcium ion per subunit.
CC -!- SUBCELLULAR LOCATION: Membrane-associated.
CC -!- MISCELLANEOUS: Group II Phospholipase A2 is found in many cells
and also extracellularly. The membrane-bound and secreted forms
are identical and are encoded by a single gene.
CC -!- SIMILARITY: Belongs to the phospholipase A2 family.

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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

CC DR EMBL; M2430; AAA36550.1; -;
DR EMBL; M2431; AAA36549.1; -;
DR EMBL; BC005919; AAH05919.1; -;
DR PIR; A32862; PSUYIF;
DR PDB; 1AYP; 31-JUL-95;
DR IUBB; 1BBC; 31-OCT-93.

CC DR PDB; 1POD; 31-OCT-93;
DR PDB; 1POE; 31-OCT-93;
DR PDB; 1KVO; 07-JUL-97;
DR PDB; 1DB4; 12-NOV-99;
DR PDB; 1DCV; 12-NOV-99;
DR Genew; HGNC:9031; PLA2G2A.
DR MIM; 172411; -;
DR GO; GO:0004623; F:phospholipase A2 activity; TAS.
DR Interpro; IPR001211; PhospholipaseA2.
DR Pfam; PF0068; phoslip; 1.
DR PRINTS; PRO00389; PHOSPHOLIPASEA2.
DR Prodrom; PRO00303; PHOSPHOLIPASEA2; 1.
DR SMART; SM00085; PACC; 1.
DR PROSITE; PS00118; PA2 HIS; 1.
DR PROSITE; PS00119; PA2 ASP; 1.
KW Hydrolase; Lipid degradation; Membrane; Signal; Calcium;
KW 3D-structure.

FT SIGNAL; 1 20
FT CHAIN; 21 144
FT ACT SITE; 67 67
FT DISTULID; 46 137
FT DISTULID; 48 64
FT DISTULID; 63 117
FT DISTULID; 69 144
FT DISTULID; 70 110
FT DISTULID; 79 103
FT DISTULID; 97 108
FT METAL; 47 47
FT METAL; 49 49
FT METAL; 51 51
FT METAL; 68 68
FT HELIX; 22 33
FT HELIX; 37 40
FT TURN; 41 41
FT TURN; 45 47
FT HELIX; 59 75
FT TURN; 76 78
FT STRAND; 88 91
FT TURN; 92 93
FT STRAND; 94 97
FT HELIX; 102 120
FT TURN; 121 121
FT HELIX; 122 124
FT TURN; 127 128

Query Match 49.9%; Score 360.5; DB 11; Length 144;
Best Local Similarity 55.6%; Pred. No. 5.9e-32;
Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;

QY 1 NLVQFGMIBERMTGK-SALQVNDYCGTCGGSHMPVDQTDWCHAHDCYGRLEKLGGE 59
DB 21 NLVNPHRMKLTGREALSYGFIGCHGGRRGSKPQADTRCCVTHDCYKELEKRGCG 80

QY 60 PKLEYKLFYSVERGIFCAGRFTCQLTCECDKRALCFRRNLGTNYKRYAHYPNKLCTCP 119
DB 81 TKFLSYKFSNSGSRITAKODSCRSQLCEDKAATCFARNKTYNKQYYNSMKHCRG5 140

RESULT 5
PA2_CERCE STANDARD; PRT; 120 AA.
ID PA2_CERCE P2178;
AC AC

DT DT 01-MAY-1991 (Rel. 18, Created)
DT DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE DE Phospholipase A2 (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase).
OS OS Cerastes cerastes (Horned desert viper).

RL	J. Protein Chem. 12:187-193 (1993).	FT	TURN	70	71
RN	[2] SEQUENCE OF 1-23, AND ACYLATION.	FT	STRAND	72	75
RP	RC TISSUE=Venom;	FT	HELIX	80	98
RC	MEDLINE=88298768; PubMed=3403524;	FT	TURN	99	99
RX	RA Cho W., Tomasselli A.G., Henrikson R.L., Kezdy F.J.;	FT	HELIX	100	102
RA	RT "The chemical basis for interfacial activation of monomeric phospholipases A2. Autocatalytic derivatization of the enzyme by acyl transfer from substrate.";	FT	STRAND	105	108
RT	RT	FT	TURN	109	109
RT	RT	FT	HELIX	110	110
RT	RT	FT	HELIX	113	116
RL	J. Biol. Chem. 263:11237-11241(1988).	SQ	SEQUENCE	123 AA;	13989 MW;
RN	[3]				C39986552D990D72 CRC64;
RP	CHARACTERIZATION.	Query Match	48.5%	Score 350;	DB 1;
RC	TISSUE=Venom;	Best Local Similarity	52.0%;	Pred No. 6.8e-31;	Length 123;
RX	MEDLINE=85054815; PubMed=6438084;	Matches	65;	Mismatches	4;
RA	RA Marganore J.M., Marutka G., Cho W., Welches W., Kezdy F.J.,	Gaps	3;		
RA	Heinrikson R.L.;	Indels	42;		
RA	RT "A new class of phospholipases A2 with lysine in place of aspartate				
RT	RT 49. Functional consequences for calcium and substrate binding.";				
RL	J. Biol. Chem. 259:13839-13843 (1984).				
RN	[4]				
RP	X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).				
RC	TISSUE=Venom;				
RX	MEDLINE=971166209; PubMed=9013608;				
RA	RA Han S.K., Yoon E.T., Scott D.L., Sigler P.B., Cho W.;				
RA	RA "Structural aspects of interfacial adorption. A crystallographic and				
RT	RT site-directed mutagenesis study of the phospholipase A2 from the				
RT	RT venom of Agkistrodon piscivorus piscivorus.";				
RL	J. Biol. Chem. 272:3573-3582 (1997).				
CC	- - FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-				
CC	acyl groups in 3-sn-phosphoglycerides.				
CC	- - CAPTIVITY ACTIVITY: Phosphatidylcholine + H(2)O = 1-				
CC	acylglycerophosphocholine + a fatty acid anion.				
CC	- - COFACTOR: Binds 1 calcium ion per subunit.				
CC	- - SUBUNIT: Monomer or homodimer.				
CC	- - SUBCELLULAR LOCATION: Secreted.				
CC	- - PTM: Acylation causes dimerization.				
CC	- - SIMILARITY: Belongs to the phospholipase A2 family. Group II				
CC	subfamily.				
DR	PIR: B53872; B53872.				
DR	PDB: 1VAP; 07-JUL-97.				
DR	InterPro: IPR01211; PhospholipaseA2.				
DR	PRINTS: PR00068; phoslip1.				
DR	PR00089; PHPLIPASEA2.				
DR	PRODOM: P000303; PhospholipaseA2; 1.				
DR	PROSITE: PS00119; PA2-ASP; 1.				
DR	PROSITE: PS00118; PA2-HIS; 1.				
KW	Hydrolyse; Lipid degradation; Calcium; Lipoprotein; Palmitate;				
KW	3D-structure.				
FT	ACT SITE 47 BY SIMILARITY.				
FT	ACT SITE 89 BY SIMILARITY.				
FT	DISULFID 26 116				
FT	DISULFID 28 44				
FT	DISULFID 43 95				
FT	DISULFID 49 123				
FT	DISULFID 50 88				
FT	DISULFID 57 81				
FT	DISULFID 75 86				
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FT	LIPID 7 7				
FT	LIPID 10 10				
FT	DISULFID 75 86				
FT	METAL 27 27				

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 CC or send an email to license@isb-sib.ch).

CC	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC	-I- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the CC 2-acyl groups in 3-sn-phosphoglycerides (By similarity).
CC	-I- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1- CC acylglycerophosphocholine + a fatty acid anion.
CC	-I- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC	-I- SUBCELLULAR LOCATION: Secreted (By similarity).
CC	-I- TISSUE SPECIFICITY: Expressed by the venom gland (probable).
CC	-I- SIMILARITY: Belongs to the phospholipase A2 family, Group II subfamily.
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DR	EMBL; AB07496; BAB02719; 1;
DR	IntelPro; IPR001211; PhospholipaseA2.
DR	Pfam; PF00068; Phoslip; 1.
DR	ProDom; PD000303; PHOSPHOLIPASEA2; 1.
DR	SMART; SM00085; PAC2; 1.
DR	PROSITE; PS00119; PA2-ASP; 1.
DR	PROSITE; PS00118; PA2-HIS; 1.
KW	Hydrolease; Lipid degradation; Calcium; Multigene family; Signal.
FT	SIGNAL 16
FT	CHAIN 17
FT	ACT SITE 63
FT	ACT SITE 105
FT	DISULFID 42
FT	DISULFID 44
FT	DISULFID 59
FT	DISULFID 65
FT	DISULFID 66
FT	DISULFID 73
FT	DISULFID 91
FT	METAL 43
FT	METAL 45
FT	METAL 47
FT	METAL 64
SQ	SEQUENCE 138 AA: 15703 MW; CBPBP581DD2F10 CRC6:
Qy	1 NLVQFCMVRMTGKSAL-QYNDYCGIGGSHPVDTDWCCGAHDCCYGRLEKUJCSE 59
Db	17 HLLQFRKMKXMTGKEPIVSAYAFGCGKGKGPDKDTDRCFVHDDCYGRV-TGCD 74
Qy	60 PKLEYKLYFSYERGFCAAGRITCQLTCECDKRALCFERNLGTYNRKVAYHYPNKLCTGP 119
Db	75 PRWDYTYSSENGDIYCEGDNPCPKTEVCEBCKDKAIAIFCDNLKTYKKEYMTFDIFCTDP 134
Qy	120 TPPC 123
Db	135 TEKC 138
RESULT 11	PA2Y_TRIPL STANDARD; PRT; 138 AA.
AC	Q90Y77; ID PA2A_MOUSE
DT	28-FEB-2003 (Rel. 41, Created)
DT	28-FEB-2003 (Rel. 41, Last sequence update)
DT	10-OCT-2003 (Rel. 42, Last annotation update)
DE	Phospholipase A2 isozyme PL-Y Precursor (EC 3.1.1.4)
DE	(Phosphatidylcholine 2-acetylhydrolase).
OC	Trimeresurus flavoviridis (Habu).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC	Viperida; Crotalinae; Trimeresurus.
OX	NCBI_TaxID:88087;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Chijwa T., Yamaguchi Y., Ogawa T., Deshimaru M., Nobuhisa I., Nakashima K.-I., Oca-Ueda N., Shimoigashi Y., Fukumaki Y., Hattori S., Ohno M., "Regional evolution of Trimeresurus flavoviridis venom-gland phospholipase A2 isozymes." DE
RA	10-Oct-2003 (Rel. 42, Last sequence update)
DT	15-Mar-2004 (Rel. 43, Last annotation update)
RT	membrane associated precursor (EC 3.1.1.4)
RESULTS 12	PA2A_MOUSE
ID	P31482; Q60871; AC P31482; Q60871; DT 01-JUL-1993 (Rel. 26, Created)
DB	17 HLLQFRKMKXMTGKEPIVSAYAFGCGKGKGPDKDTDRCFVHDDCYGRV-TGCD 74
Qy	60 PKLEYKLYFSYERGFCAAGRITCQLTCECDKRALCFERNLGTYNRKVAYHYPNKLCTGP 119
DB	75 PRWDYTYSSENGDIYCEGDNPCPKTEVCEBCKDKAIAIFCDNLKTYKKEYMTFDIFCTDP 134
Qy	120 TPPC 123
DB	135 TEKC 138
RESULTS 13	PA2A_MOUSE
ID	P31482; Q60871; AC P31482; Q60871; DT 01-JUL-1993 (Rel. 26, Created)
DB	75 PRWDYTYSSENGDIYCEGDNPCPKTEVCEBCKDKAIAIFCDNLKTYKKEYMTFDIFCTDP 134
Qy	120 TPPC 123
DB	135 TEKC 138

RESULT 15
 ID PA2X_TRIFL STANDARD PRT; 122 AA.
 AC PG6650;
 DT 01-JAN-1998 (Rel. 06, Created)
 DT 01-JAN-1998 (Rel. 06, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Phospholipase A2 isozyme PL-X (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase).
 OS Trimeresurus flavoviridis (Habu).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scincoglossa; Serpentes;
 OC Viperidae; Crotalinae; Trimeresurus.
 NCBI_TaxID=88087;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=87179112; PubMed=3564060;
 RA Kini R.M., Kawabata S.-I., Iwanaga S.;
 RT "Comparison of amino terminal region of three isoenzymes of
 phospholipases A2 (PL-Ia, PL-IIa, PL-X) from Trimeresurus
 flavoviridis (habu snake) venom and the complete amino acid sequence
 of the basic phospholipase, PL-X.";
 RL Toxicon 24:1117-1129(1986).
 CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides.
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H₂O = 1-acylglycerophosphocholine + a fatty acid anion.
 CC -!- COFACTOR: Binds 1 calcium ion per subunit (BY similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- SIMILARITY: Belongs to the phospholipase A2 family. Group II subfamily.
 DR PIR: A25500; PSTVXF.
 DR HSSP; P51972; IVAP.
 DR InterPro: IPR001211; PhospholipaseA2.
 DR Pfam: PF00068; Phoslip; 1.
 DR PRINTS; PR0389; PHOSPHOLIPASEA2.
 DR ProDom; PD000303; BhsopholipaseA2; 1.
 DR SMART; SM00085; PACC; 1.
 DR PROSITE; PS000119; PA2-ASP; FALSE_NEG.
 DR PROSITE; PS000118; PA2-HIS; 1.
 KW Hydrolase; Lipid degradation; Calcium; Multigene family.
 FT ACT_SITE 47 47 BY SIMILARITY.
 FT ACT_SITE 89 89 BY SIMILARITY.
 FT DISULFID 26 28 BY SIMILARITY.
 FT METAL 26 28 BY SIMILARITY.
 FT METAL 28 28 BY SIMILARITY.
 FT METAL 30 30 BY SIMILARITY.
 FT METAL 47 47 CALCIUM (BY SIMILARITY).
 SQ SEQUENCE 121 AA; 13363 MW; DC0500087839E504 CRC64;
 Query Match 47.1%; Score 340; DB 1; Length 121;
 Best Local Similarity 47.2%; Pred. No. 8e-30; Gaps 1;
 Matches 58; Conservative 15; Mismatches 48; Indels 2; Gaps 1;
 SEQ SEQUENCE 122 AA; 13981 MW; A9D652276C5DDFO CRC64;
 Query Match 47.0%; Score 339.5; DB 1; Length 122;
 Best Local Similarity 49.2%; Pred. No. 9.2e-30; Gaps 2;
 Matches 61; Conservative 16; Mismatches 44; Indels 3; Gaps 2;
 Qy 1 NLVQFGMVKMTGKSLQNDYCGYCQGSHMPDQTWCCHAHDCCYGRLEKGCPE 60
 Db 1 NLIQGNMISAMTGHSSLLAYASGYCGWNGKGQPKDDDTDRCCFVHDCCYGRADK--CSP 58
 Qy 61 KLEKYLFSVERGLFCAGRITTCQRLLTCECDKRAALCPRNLGTNRYKTAHYPNKLCTGPT 120
 Db 59 KMILYSYKFHNGNIVCGDKNACKKVCECDRVAICFAASKHSYNKNLWRYPSSSKCTGTA 118
 Qy 121 PPC 123
 Db 119 EKC 121
 DR 59 PWKSYTYSLENGDIVCGDPYCTRKVCEDKAATCPDNLKTYKONSYMTPDIFCDP 118
 DR 59 PWKSYTYSLENGDIVCGDPYCTRKVCEDKAATCPDNLKTYKONSYMTPDIFCDP 118
 DR 120 TPPC 123
 Db 119 TEPC 122

Search completed: July 3, 2004, 05:16:40
 Job time : 9.81887 secs

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OM protein - protein search, using sw mode.

Run on: July 3, 2004, 05:15:00 ; Search time 12.5321 seconds
 (without alignments)

506.699 Million cell updates/sec

Title: US-10-088-092A-30_COPY_20_142

Perfect score: 722

Sequence: 1 NLVQGVMIEKMTGKSALQY.....YNRKVAYHYPNKLCTGPTPPC 123

Scoring table: BL0SUM62

GAPDP 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database : Issued Patents AA:
 1: /cn2_6_ptodata/2/iaa/5a_COMB.pep:
 2: /cn2_6_ptodata/2/iaa/5b_COMB.pep:
 3: /cn2_6_ptodata/2/iaa/6a_COMB.pep:
 4: /cn2_6_ptodata/2/iaa/6b_COMB.pep:
 5: /cn2_6_ptodata/2/iaa/BCTUS_Comb.pep:
 6: /cn2_6_ptodata/2/iaa/backFiles1.pep:
 *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	360.5	360.5	49.9	124	1	US-08-170-360-4
2	360.5	45.9	124	2	US-08-888-497-39	Sequence 4, Appl
3	360.5	49.9	124	4	US-09-362-230-39	Sequence 39, Appl
4	360.5	49.9	124	4	US-09-740-569-2	Sequence 39, Appl
5	360.5	49.9	124	5	PCT-US94-07926-39	Sequence 39, Appl
6	360.5	49.9	144	1	US-08-186-895-10	Sequence 10, Appl
7	360.5	49.9	144	2	US-08-188-497-37	Sequence 37, Appl
8	360.5	49.9	144	2	US-09-362-230-37	Sequence 39, Appl
9	360.5	49.9	144	5	PCT-US94-07926-37	Sequence 37, Appl
10	348	48.2	125	2	US-08-888-497-42	Sequence 42, Appl
11	348	48.2	125	4	US-09-362-230-42	Sequence 42, Appl
12	348	48.2	125	5	PCT-US94-07926-42	Sequence 42, Appl
13	348	48.2	146	4	US-08-888-497-35	Sequence 35, Appl
14	348	48.2	146	4	US-09-362-230-35	Sequence 35, Appl
15	348	48.2	146	5	PCT-US94-07926-35	Sequence 35, Appl
16	341	47.2	146	3	US-08-966-317-3	Sequence 3, Appl
17	341	47.2	146	4	US-09-489-770-3	Sequence 3, Appl
18	337	46.7	146	3	US-08-966-317-4	Sequence 4, Appl
19	337	46.7	146	4	US-09-489-770-4	Sequence 4, Appl
20	321	44.5	125	1	US-08-170-360-5	Sequence 5, Appl
21	299.5	41.5	118	2	US-08-497-40	Sequence 4, Appl
22	299.5	41.5	118	4	US-09-097-094-5	Sequence 5, Appl
23	299.5	41.5	118	4	US-09-362-230-40	Sequence 40, Appl
24	299.5	41.5	118	5	PCT-US94-07926-40	Sequence 40, Appl
25	299.5	41.5	122	1	US-07-734-534A-1	Sequence 1, Appl
26	299.5	41.5	138	2	US-08-888-497-32	Sequence 32, Appl
27	299.5	41.5	138	4	US-09-362-230-32	Sequence 32, Appl

RESULT 1
 US-08-170-360-4

; Sequence 4, Application US/08170360

; Patent No. 5656602

; GENERAL INFORMATION:

; APPLICANT: Tseng, Albert P. S. -

; TITLE OF INVENTION: PLA2 INHIBITORY COMPOUNDS

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Rothwell, Figg, Ernst & Kurz

; STREET: Suite 701-E, 555 Thirteenth St., N.W.

; CITY: Washington

; STATE: D. C.

; COUNTRY: U.S.A.

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/170-360

; FILING DATE: 03-MAR-1994

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: AU PCT/AU92/00333

; FILING DATE: 06-JUL-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: AU PK 7058

; FILING DATE: 04-JUL-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Ernst, Barbara G.

; REGISTRATION NUMBER: 30,377

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)783-5640

; TELEX/FAX: (202)783-6031

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 124 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: N-terminal

; US-08-170-360-4

ALIGNMENTS

1997 (Issued)

Query Match 49.9%; Score 360.5; DB 1; Length 124;
 Best Local Similarity 55.6%; Pred. No. 1.3e-31; Gaps 1;
 Matches 69; Conservative 9; Mismatches 45; Indels 1;

Qy 1 NLVQFGVMIEKMTGK-SALQYNDGCGYCGIGGSHWPVQDTCWCCAHDCCYGRLEKLGCE 59
 Db 1 NLVNPHRMILKTTGGEAALSYGFTGCHCGVGGRSPKATDRCCVTHDOCYKRLERCG 60

Qy 60 PKLEYKLFYSERGIFCAGRTTCAQRLLCTCEDIKRALCFRRNLGTYNRKYAHYPNKLCTGP 119
 Db 61 TKFLSYKFNSGSRITCAKODSRSQLCBODKAATCFARNKTYNKQYYSNKHCRGS 120

Qy 120 TPPC 123
 Db 121 TPRC 124

RESULT 3 US-09-362-230-39
 Sequence 39, Application US/09362230
 Patent No. 6352849

GENERAL INFORMATION:
 APPLICANT: Seilhamer, Jeffrey J.
 ADDRESS: Ruden, Barnett, McClosky, Smith, Schuster &
 STREET: 200 East Broward Boulevard
 CITY: Fort Lauderdale
 STATE: FL
 COUNTRY: USA
 ZIP: 33301

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/362,230
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/888,497
 ATTORNEY/AGENT INFORMATION:
 NAME: Manso, Peter J.
 REGISTRATION NUMBER: 32,264
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 305-527-2998
 TELEFAX: 305-764-4996
 INFORMATION FOR SEQ ID NO: 39:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 124 amino acids
 STRANDEDNESS: single
 TOPOLOGY: Linear
 MOLECULE TYPE: protein

US-09-362-230-39

Query Match 49.9%; Score 360.5; DB 4; Length 124;
 Best Local Similarity 55.6%; Pred. No. 1.3e-31; Gaps 1;
 Matches 69; Conservative 9; Mismatches 45; Indels 1;

Qy 1 NLVQFGVMIEKMTGK-SALQYNDGCGYCGIGGSHWPVQDTCWCCAHDCCYGRLEKLGCE 59
 Db 1 NLVNPHRMILKTTGGEAALSYGFTGCHCGVGGRSPKATDRCCVTHDOCYKRLERCG 60

Qy 60 PKLEYKLFYSERGIFCAGRTTCAQRLLCTCEDIKRALCFRRNLGTYNRKYAHYPNKLCTGP 119
 Db 61 TKFLSYKFNSGSRITCAKODSRSQLCBODKAATCFARNKTYNKQYYSNKHCRGS 120

TELEX: 6714627 CUSH
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 144 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-001-186-895-10

Query Match 49.9%; Score 360.5; DB 1; Length 144;
 Best Local Similarity 55.6%; Pred. No. 1.5e-31;
 Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;

Qy 1 NLVQFQVMERMTGK-SALOYNDIGCYCGGSSWMPVQDTWCCHAHDCIGRLKEKGCE 59
 Db 21 NLVNPHRMKLTGKEAALSYGFGCHGCGGRGSPKDATDRCCTVHDCCYRLEKRGCG 80

Qy 60 PKLERYLFYSERGLFCAGRTTCORLTCEDKAALCFPRNLGTYNRYAHYPNKLCTGP 119
 Db 81 TKEFSYKFNSGSRITCAKDSCRSQLCEDKAATACTFARNKTYTNYKQYISNMKHFGS 140

Qy 120 TPPC 123
 Db 141 TPRC 144

RESULT 8
 US-09-362-230-37
 / Sequence 37, Application US/09362230
 / Patent No. 6352849

/ GENERAL INFORMATION:
 / APPLICANT: Tischfield, Jay A.
 / APPLICANT: Seilhamer, Jeffrey J.
 / TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide Sequences and Low Molecular Weight Amino Acid Sequences
 / SEQUENCES AND LOW MOLECULAR WEIGHT AMINO ACID SEQUENCES
 / SEQUENCES AND NUCLEOTIDE SEQUENCES
 / ENCODED THEREBY, ANTISENSE SEQUENCES AND NUCLEOTIDE SEQUENCES HAVING INTERNAL RIBOSOME BINDING SITES

/ NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:
 ADDRESS: Rudea, Barnett, McClosky, Smith, Schuster &
 ADDRESS: Russell, PA
 STREET: 200 East Broward Boulevard
 CITY: Fort Lauderdale
 STATE: FL
 ZIP: 33301

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patient In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/888,497
 FILING DATE:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/651,405
 FILING DATE:
 APPLICATION NUMBER: US/08/097,354
 FILING DATE: 26-JUL-1993

REGISTRATION NUMBER: 32,264
 NAME: Manso, Peter J.
 REGISTRATION NUMBER: 32,264
 REFERENCE/DOCKET NUMBER: IN21044-5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 305-764-4996
 TELEFAX: 305-764-4996

INFORMATION FOR SEQ ID NO: 37:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 144 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-362-230-37

Query Match 49.9%; Score 360.5; DB 4; Length 144;
 Best Local Similarity 55.6%; Pred. No. 1.5e-31;
 Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;

Qy 1 NLVQFGMIEKMTGK-SALQNDYGGCIGGSHWPVDOTWCCHAHDCCYGRLEKLGCE 59
 | ||||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 21 NLVNFRMIIKTTGKEAALSSGYGCHGVPDKATRCVTHDCCYKRLERKGCG 80

Qy 60 PKEKYLFSVSRGIFCAAGRITCQRLTCEDKRAAICFRRNLGTYNRKYAHYPNKLCTGP 119
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 81 TKPLSTKFSNSGSRITCAKQDSRCLCECDAAAATCFARNKTTYNKCYQYSNKHCRGS 140

Qy 120 TPPC 123
 Db 141 TPRC 144

RESULT 9 PCT-US94-07926-37
 ; GENERAL INFORMATION:
 ; APPLICANT: Tischfield, Jay A.
 ; ADDRESS: Ruden, Barnett, McClosky, Smith, Schuster &
 ; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide Sequences and Low Molecular Weight Amino Acid Sequences
 ; SEQUENCE NUMBER: US-08-497-42, Application US/08888497
 ; PATENT NUMBER: 5972677
 ; GENERAL INFORMATION:
 ; APPLICANT: Seilhamer, Jeffrey J.
 ; ADDRESS: Russel PA
 ; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide Sequences Having Internal Ribosome Binding Sites
 ; SEQUENCE NUMBER: US-08-497-42, Application US/08888497
 ; CORRESPONDENCE ADDRESS:
 ; ZIP: 33301
 ; CITY: Fort Lauderdale
 ; STATE: FL
 ; COUNTRY: USA
 ; NUMBER OF SEQUENCES: 44
 ; CITY: Fort Lauderdale
 ; STATE: FL
 ; COUNTRY: USA
 ; ZIP: 33301
 ; COMPUTER READABLE FORM:
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; PRIORITY DATA:
 ; APPLICATION NUMBER: PCT/US94/07926
 ; FILING DATE: 15-JUL-1994
 ; CLASSIFICATION:
 ; PRIORITY DATA:
 ; APPLICATION NUMBER: US 08/097, 354
 ; FILING DATE: 26-JUL-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Manso, Peter J.
 ; REGISTRATION NUMBER: 32, 264
 ; REFERENCE DOCKET NUMBER: IN21044-5
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 305-527-2498
 ; TELEFAX: 305-764-4996
 ; INFORMATION FOR SEQ ID NO: 42:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 125 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 144 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 PCT-US94-07926-37

Query Match 1 NLVQFGMIEKMTGKSA-LQYNDYGGCIGGSHWPVDOTWCCHAHDCCYGRLEKLGCE 59
 Best Local Similarity 1 SLLERQMLFKTGRADYSVGFNGCHGGRSPKDAIDWCCVTHDCYNRLEKRGCG 60
 Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;

Qy 1 NLVQFGMIEKMTGK-SALQNDYGGCIGGSHWPVDOTWCCHAHDCCYGRLEKLGCE 59
 Db 21 NLVNFRMIIKTTGKEAALSSGYGCHGVPDKATRCVTHDCCYKRLERKGCG 80

Qy 60 PKEKYLFSVSRGIFCAAGRITCQRLTCEDKRAAICFRRNLGTYNRKYAHYPNKLCTGP 119
 Db 81 TKPLSTKFSNSGSRITCAKQDSRCLCECDAAAATCFARNKTTYNKCYQYSNKHCRGS 140

RESULT 11

US-09-362-230-42
Sequence 42, Application US/09362230
GENERAL INFORMATION:
Patent No. 652849
APPLICANT: Tischfield, Jay A.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Therby, Antisense Sequences and Nucleotide Binding Sites
TITLE OF INVENTION: Encoded Therby, Antisense Sequences and Nucleotide Binding Sites
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & Tischfield, Jeffrey J.
STREET: 200 East Broward Boulevard
STATE: FL
COUNTRY: USA
ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/362,230
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/888,497
FILING DATE:
APPLICATION NUMBER: US 08/097,354
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/362,230
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/888,497
FILING DATE:
APPLICATION NUMBER: US 08/097,354
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-764-4956
TELEFAX: 305-764-4956
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-07926-42

Qy Query Match 48.2%; Score 348; DB 5; Length 125;
Best Local Similarity 51.2%; Pred. No. 2.9e-30;
Matches 64; Conservative 14; Mismatches 45; Indels 2; Gaps 2;

Db 1 NLVQFGVMIEKMTGKSA-LOYNDYGCYCGIGGSHPVDOTDWCHAHCCYGRBLRGCE 59
1 SLLFPQMLFKTGGRADYSYGFGCHCCGGRGSXPATDWCCVTHCCYNNLERKSCG 60

Qy 60 PRLEYKLFYSVERGIFCA-GRTTCORLTCDKHALCFPRNLTGYNKAYPNKLCTG 118
61 TKFVTYKFSTYRGQIISCSNTQDSCKQLCQCDRAAECFARNKSKSYLKQYPNKEKG 120

Db 61 TKEVYKFSYRGQIISCSNTQDSCKQLCQCDRAAECFARNKSKSYLKQYPNKEKG 120

RESULT 13
US-08-888-497-35
Sequence 35, Application US/08888497
Patent No. 597267
GENERAL INFORMATION:
APPLICANT: Tischfield, Jay A.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Therby, Antisense Sequences and Nucleotide Binding Sites
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & Tischfield, Jeffrey J.
STREET: 200 East Broward Boulevard

RESULT 12
PCT-US94-07926-42
GENERAL INFORMATION:
SEQUENCE 42, Application PC/TUS9407926
APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Therby, Antisense Sequences and Nucleotide Binding Sites
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & Tischfield, Jeffrey J.
STREET: 200 East Broward Boulevard

CITY: Fort Lauderdale
 STATE: FL
 COUNTRY: USA
 ZIP: 33301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 FILING DATE:
 APPLICATION NUMBER: US/08/888, 497
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/651, 405
 FILING DATE:
 APPLICATION NUMBER: US 08/097, 354
 FILING DATE: 26-JUL-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Manso, Peter J.
 REGISTRATION NUMBER: 32, 264
 REFERENCE/DOCKET NUMBER: IN21044-5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 305-527-2438
 TELEFAX: 305-764-4996
 INFORMATION FOR SEQ ID NO: 35:
 LENGTH: 146 amino acids
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-888-497-35
 SEQUENCE CHARACTERISTICS:
 LENGTH: 146 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-888-497-35

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/362, 230
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/888, 497
 FILING DATE:
 APPLICATION NUMBER: US 08/097, 354
 FILING DATE: 26-JUL-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Manso, Peter J.
 REGISTRATION NUMBER: 32, 264
 REFERENCE/DOCKET NUMBER: IN21044-5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 305-527-2438
 TELEFAX: 305-764-4996
 INFORMATION FOR SEQ ID NO: 35:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 146 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-362-230-35
 Query Match Score 48.2%; Score 348; DB 4; Length 146;
 Best Local Similarity 51.2%; Pred. No. 3.5e-30;
 Matches 64; Conservative 14; Mismatches 45; Indels 2; Gaps 2;
 Qy 1 NLVQFGVMERMTGKSA-LQYNDGCGTGGSHMPVDTDWCCCHAHDCCYGRLRKLGCE 59
 Db 22 SLLFGQMILFKTKRADSYGFYGGCHGCGYGRGSPKDADWCCVTHDCCYNRLEKRKGCG 81
 Qy 60 PKELEYLFVSERGIFCA-GRTTCORLTCECDKRAALCFRRNLGTYNRKYAHYPNKLCTG 118
 Db 82 TKFVTYKFSTYRGQIQCSTNQDSCKQLCQCDKAEECFARNKKSYSLKQFYPNPKCKG 141
 RESULT 15
 PCT-US4-07926-15
 Sequence 35, Application PC/TUS9407926
 GENERAL INFORMATION:
 APPLICANT: Tischfield, Jay A.
 ADDRESS: Seilhamer, Jeffrey J.
 TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide Sequences and Low Molecular Weight Amino Acid Sequences
 TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide Sequences Having Internal Ribosome Binding Sites
 NUMBER OF SEQUENCES: 44
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & Zupp
 ADDRESS: Russell PA
 STREET: 200 East Broward Boulevard
 CITY: Fort Lauderdale
 STATE: FL
 COUNTRY: USA
 ZIP: 33301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/07926
 FILING DATE: 15-JUL-1994
 CLASSIFICATION:

RESULT 14
 US-09-362-230-35
 Sequence 35, Application US/09362230
 Patent No. 632849
 GENERAL INFORMATION:
 APPLICANT: Tischfield, Jay A.
 ADDRESS: Seilhamer, Jeffrey J.
 TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide Sequences and Low Molecular Weight Amino Acid Sequences
 TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide Sequences Having Internal Ribosome Binding Sites
 NUMBER OF SEQUENCES: 44
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & Zupp
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 COUNTRY: USA
 ZIP: 33301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/097,354
 FILING DATE: 26-JUL-1993
 ATTORNEY/AGENT INFORMATION:
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 REGISTRATION NUMBER: 32,264
 REFERENCE/DOCKET NUMBER: IN21044-5
 TELECOMMUNICATION INFORMATION:
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 INFORMATION FOR SEQ ID NO: 35:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 146 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US94-07926-35

Query Match Score 348 DB 5; Length 146;
 Best Local Similarity 48.2%; Pred. No. 3.5e-30;
 Matches 51.2%; Pred. No. 3.5e-30;
 保守性 14; Mismatches 45; Indels 2; Gaps 2;
 Matches 64; Conservative 14; Mismatches 45;

Qy	1 NLVQFGVMIKMKGKSA-LOYNNDGCGYCIGGGSHMPVDOTDWCCCHAHDCCYGRLEKLIGCE	59
Db	22 SLLFGQMILFKTGFADYSGFVGCHCGGGRESPOATDWCCVTHDCYDNLERRGCG	81
Qy	60 PKLEYKLFPSYSERGIFCA-GRTTCORLTCECDKSAALCFRNLGTYNRKVAHYPNKLCTG	118
Db	82 TRKFVTYKFSYRGQQISCSNTQDSCKQLCQCDRAAECPARNKSYSLRYQFYPNKECKG	141
Qy	119 PTPPC 123	
Db	142 KTPSC 146	

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